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(54) Title: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND METHODS FOR THEIR USE (57) Abstract Compounds and methods for diagnosing prostate cancer are provided. The inventive compounds include polypeptides containing at least a portion of a prostate tumor protein. The inventive polypeptides may be used to generate antibodies useful for the diagnosis and monitoring of prostate cancer. Nucleic acid sequences for preparing probes, primers, and polypeptides are also provided.		

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COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND METHODS FOR THEIR USE

TECHNICAL FIELD

The present invention relates generally to the treatment and monitoring of prostate cancer. The invention is more particularly related to polypeptides comprising at least a portion of a prostate protein. Such polypeptides may be used for the production of compounds, such as antibodies, useful for diagnosing and monitoring the progression of prostate cancer, and possibly other tumor types, in a patient.

BACKGROUND OF THE INVENTION

Prostate cancer is the most common form of cancer among males, with an estimated incidence of 30% in men over the age of 50. Overwhelming clinical evidence shows that human prostate cancer has the propensity to metastasize to bone, and the disease appears to progress inevitably from androgen dependent to androgen refractory status, leading to increased patient mortality. This prevalent disease is currently the second leading cause of cancer death among men in the U.S.

In spite of considerable research into diagnosis and therapy of the disease, prostate cancer remains difficult to detect and to treat. Commonly, treatment is based on surgery and/or radiation therapy, but these methods are ineffective in a significant percentage of cases. Two previously identified prostate specific proteins - prostate specific antigen (PSA) and prostatic acid phosphatase (PAP) - have limited diagnostic and therapeutic potential. For example, PSA levels do not always correlate well with the presence of prostate cancer, being positive in a percentage of non-prostate cancer cases, including benign prostatic hyperplasia (BPH). Furthermore, PSA measurements correlate with prostate volume, and do not indicate the level of metastasis.

Accordingly, there remains a need in the art for improved and diagnostic methods for prostate cancer.

SUMMARY OF THE INVENTION

The present invention provides methods for immunodiagnosis of prostate cancer, together with kits for use in such methods. Polypeptides are disclosed which comprise at least an immunogenic portion of a prostate tumor protein or a variant of said protein that differs only in conservative substitutions and/or modifications, wherein the prostate tumor protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-11, 115-171, 173-175, 177, 179-224 and variants thereof. Such polypeptides may be usefully employed in the diagnosis and monitoring of prostate cancer.

In one specific aspect of the present invention, methods are provided for detecting prostate cancer in a patient, comprising: (a) contacting a biological sample obtained from a patient with a binding agent that is capable of binding to one of the above polypeptides; and (b) detecting in the sample a protein or polypeptide that binds to the binding agent. In preferred embodiments, the binding agent is an antibody, most preferably a monoclonal antibody.

In related aspects, methods are provided for monitoring the progression of prostate cancer in a patient, comprising: (a) contacting a biological sample obtained from a patient with a binding agent that is capable of binding to one of the above polypeptides; (b) determining in the sample an amount of a protein or polypeptide that binds to the binding agent; (c) repeating steps (a) and (b); and comparing the amounts of polypeptide detected in steps (b) and (c).

Within related aspects, the present invention provides antibodies, preferably monoclonal antibodies, that bind to the inventive polypeptides, as well as diagnostic kits comprising such antibodies, and methods of using such antibodies to inhibit the development of prostate cancer.

The present invention further provides methods for detecting prostate cancer comprising: (a) obtaining a biological sample from a patient; (b) contacting the sample with a first and a second oligonucleotide primer in a polymerase chain reaction, at least one of the oligonucleotide primers being specific for a DNA molecule that encodes one of the above polypeptides; and (c) detecting in the sample a DNA sequence that amplifies in the presence of the first and second oligonucleotide primers. In a preferred embodiment, at least one of the

oligonucleotide primers comprises at least about 10 contiguous nucleotides of a DNA molecule having a partial sequence selected from the group consisting of SEQ ID Nos: 2-3, 5-107, 109-11, 115-171, 173-175, 177 and 179-224.

In a further aspect, the present invention provides a method for detecting prostate cancer in a patient comprising: (a) obtaining a biological sample from the patient; (b) contacting the sample with an oligonucleotide probe specific for a DNA molecule that encodes one of the above polypeptides; and (c) detecting in the sample a DNA sequence that hybridizes to the oligonucleotide probe. Preferably, the oligonucleotide probe comprises at least about 15 contiguous nucleotides of a DNA molecule having a partial sequence selected from the group consisting of SEQ ID Nos: 2-3, 5-107, 109-11, 115-171, 173-175, 177 and 179-224.

In related aspects, diagnostic kits comprising the above oligonucleotide probes or primers are provided.

These and other aspects of the present invention will become apparent upon reference to the following detailed description and attached drawings. All references disclosed herein are hereby incorporated by reference in their entirety as if each was incorporated individually.

DETAILED DESCRIPTION OF THE INVENTION

As noted above, the present invention is generally directed to compositions and methods for the immunodiagnosis and monitoring of prostate cancer. The inventive compositions are generally polypeptides that comprise at least a portion of a prostate tumor protein. Also included within the present invention are molecules (such as an antibody or fragment thereof) that bind to the inventive polypeptides. Such molecules are referred to herein as "binding agents."

In particular, the subject invention discloses polypeptides comprising at least a portion of a human prostate tumor protein, or a variant thereof such a protein, wherein the prostate tumor protein includes an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-11, 115-171, 173-175, 177, 179-224, the complements of said nucleotide sequences and variants thereof. As used herein, the term "polypeptide"

encompasses amino acid chains of any length, including full length proteins, wherein the amino acid residues are linked by covalent peptide bonds. Thus, a polypeptide comprising a portion of one of the above prostate proteins may consist entirely of the portion, or the portion may be present within a larger polypeptide that contains additional sequences. The additional sequences may be derived from the native protein or may be heterologous, and such sequences may be immunoreactive and/or antigenic.

As used herein, an "immunogenic portion" of a human prostate tumor protein is a portion that is capable of eliciting an immune response in a patient inflicted with prostate cancer and as such binds to antibodies present within sera from a prostate cancer patient. Immunogenic portions of the proteins described herein may thus be identified in antibody binding assays. Such assays may generally be performed using any of a variety of means known to those of ordinary skill in the art, as described, for example, in Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, 1988. For example, a polypeptide may be immobilized on a solid support (as described below) and contacted with patient sera to allow binding of antibodies within the sera to the immobilized polypeptide. Unbound sera may then be removed and bound antibodies detected using, for example, ¹²⁵I-labeled Protein A. Alternatively, a polypeptide may be used to generate monoclonal and polyclonal antibodies for use in detection of the polypeptide in blood or other fluids of prostate cancer patients.

The compositions and methods of the present invention also encompass variants of the above polypeptides and DNA molecules. A polypeptide "variant," as used herein, is a polypeptide that differs from the recited polypeptide only in conservative substitutions and/or modifications, such that the therapeutic, antigenic and/or immunogenic properties of the polypeptide are retained. Polypeptide variants preferably exhibit at least about 70%, more preferably at least about 90% and most preferably at least about 95% identity to the identified polypeptides. For prostate tumor polypeptides with immunoreactive properties, variants may, alternatively, be identified by modifying the amino acid sequence of one of the above polypeptides, and evaluating the immunoreactivity of the modified polypeptide. For prostate tumor polypeptides useful for the generation of diagnostic binding agents, a variant may be identified by evaluating a modified polypeptide for the ability to

generate antibodies that detect the presence or absence of prostate cancer. Such modified sequences may be prepared and tested using, for example, the representative procedures described herein.

As used herein, a "conservative substitution" is one in which an amino acid is substituted for another amino acid that has similar properties, such that one skilled in the art of peptide chemistry would expect the secondary structure and hydrophobic nature of the polypeptide to be substantially unchanged. In general, the following groups of amino acids represent conservative changes: (1) ala, pro, gly, glu, asp, gln, asn, ser, thr; (2) cys, ser, tyr, thr; (3) val, ile, leu, met, ala, phe; (4) lys, arg, his; and (5) phe, tyr, trp, his.

Variants may also, or alternatively, contain other modifications, including the deletion or addition of amino acids that have minimal influence on the antigenic properties, secondary structure and hydrophobic nature of the polypeptide. For example, a polypeptide may be conjugated to a signal (or leader) sequence at the N-terminal end of the protein which co-translationally or post-translationally directs transfer of the protein. The polypeptide may also be conjugated to a linker or other sequence for ease of synthesis, purification or identification of the polypeptide (*e.g.*, poly-His), or to enhance binding of the polypeptide to a solid support. For example, a polypeptide may be conjugated to an immunoglobulin Fc region.

A nucleotide "variant" is a sequence that differs from the recited nucleotide sequence in having one or more nucleotide deletions, substitutions or additions. Such modifications may be readily introduced using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis as taught, for example, by Adelman et al. (*DNA*, 2:183, 1983). Nucleotide variants may be naturally occurring allelic variants, or non-naturally occurring variants. Variant nucleotide sequences preferably exhibit at least about 70%, more preferably at least about 80% and most preferably at least about 90% identity to the recited sequence. Such variant nucleotide sequences will generally hybridize to the recited nucleotide sequence under stringent conditions. As used herein, "stringent conditions" refers to prewashing in a solution of 6X SSC, 0.2% SDS; hybridizing at 65 °C, 6X SSC, 0.2% SDS overnight; followed by two washes of 30 minutes each in 1X SSC, 0.1% SDS at 65 °C and two washes of 30 minutes each in 0.2X SSC, 0.1% SDS at 65 °C.

"Polypeptides" as used herein also include combination, or fusion, polypeptides. A "combination polypeptide" is a polypeptide comprising at least one of the above immunogenic portions and one or more additional immunogenic prostate tumor-specific sequences, which are joined via a peptide linkage into a single amino acid chain. The sequences may be joined directly (*i.e.*, with no intervening amino acids) or may be joined by way of a linked sequence (*e.g.*, Gly-Cys-Gly) that does not significantly diminish the immunogenic properties of the component polypeptides.

The prostate tumor proteins of the present invention, and DNA molecules encoding such proteins, may be isolated from prostate tumor tissue using any of a variety of methods well known in the art. DNA sequences corresponding to a gene (of a portion thereof) encoding one of the inventive prostate tumor proteins may be isolated from a prostate tumor cDNA library using a subtraction technique as described in detail below. Examples of such DNA sequences are provided in SEQ ID Nos: 1-107, 109-111, 115-171, 173-175, 177 and 179-224. Partial DNA sequences thus obtained may be used to design oligonucleotide primers for the amplification of full-length DNA sequences in a polymerase chain reaction (PCR), using techniques well known in the art (see, for example, Mullis et al., *Cold Spring Harbor Symp. Quant. Biol.*, 51:263, 1987; Erlich ed., *PCR Technology*, Stockton Press, NY, 1989). Once a DNA sequence encoding a polypeptide is obtained, any of the above modifications may be readily introduced using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis as taught, for example, by Adelman et al. (*DNA*, 2:183, 1983).

The prostate tumor polypeptides disclosed herein may also be generated by synthetic or recombinant means. Synthetic polypeptides having fewer than about 100 amino acids, and generally fewer than about 50 amino acids, may be generated using techniques well known to those of ordinary skill in the art. For example, such polypeptides may be synthesized using any of the commercially available solid-phase techniques, such as the Merrifield solid-phase synthesis method, where amino acids are sequentially added to a growing amino acid chain (see, for example, Merrifield, *J. Am. Chem. Soc.* 85:2149-2146, 1963). Equipment for automated synthesis of polypeptides is commercially available from

suppliers such as Perkin Elmer/Applied BioSystems Division (Foster City, CA), and may be operated according to the manufacturer's instructions.

Alternatively, any of the above polypeptides may be produced recombinantly by inserting a DNA sequence that encodes the polypeptide into an expression vector and expressing the protein in an appropriate host. Any of a variety of expression vectors known to those of ordinary skill in the art may be employed to express recombinant polypeptides of this invention. Expression may be achieved in any appropriate host cell that has been transformed or transfected with an expression vector containing a DNA molecule that encodes a recombinant polypeptide. Suitable host cells include prokaryotes, yeast and higher eukaryotic cells. Preferably, the host cells employed are *E. coli*, yeast or a mammalian cell line, such as CHO cells. The DNA sequences expressed in this manner may encode naturally occurring polypeptides, portions of naturally occurring polypeptides, or other variants thereof.

In general, regardless of the method of preparation, the polypeptides disclosed herein are prepared in substantially pure form (*i.e.*, the polypeptides are homogenous as determined by amino acid composition and primary sequence analysis). Preferably, the polypeptides are at least about 90% pure, more preferably at least about 95% pure and most preferably at least about 99% pure. In certain embodiments, described in more detail below, the substantially pure polypeptides are incorporated into pharmaceutical compositions or vaccines for use in one or more of the methods disclosed herein.

In a related aspect, the present invention provides fusion proteins comprising a first and a second inventive polypeptide or, alternatively, a polypeptide of the present invention and a known prostate antigen, together with variants of such fusion proteins. The fusion proteins of the present invention may also include a linker peptide between the first and second polypeptides.

A DNA sequence encoding a fusion protein of the present invention is constructed using known recombinant DNA techniques to assemble separate DNA sequences encoding the first and second polypeptides into an appropriate expression vector. The 3' end of a DNA sequence encoding the first polypeptide is ligated, with or without a peptide linker, to the 5' end of a DNA sequence encoding the second polypeptide so that the reading frames

of the sequences are in phase to permit mRNA translation of the two DNA sequences into a single fusion protein that retains the biological activity of both the first and the second polypeptides.

A peptide linker sequence may be employed to separate the first and the second polypeptides by a distance sufficient to ensure that each polypeptide folds into its secondary and tertiary structures. Such a peptide linker sequence is incorporated into the fusion protein using standard techniques well known in the art. Suitable peptide linker sequences may be chosen based on the following factors: (1) their ability to adopt a flexible extended conformation; (2) their inability to adopt a secondary structure that could interact with functional epitopes on the first and second polypeptides; and (3) the lack of hydrophobic or charged residues that might react with the polypeptide functional epitopes. Preferred peptide linker sequences contain Gly, Asn and Ser residues. Other near neutral amino acids, such as Thr and Ala may also be used in the linker sequence. Amino acid sequences which may be usefully employed as linkers include those disclosed in Maratea et al., *Gene* 40:39-46, 1985; Murphy et al., *Proc. Natl. Acad. Sci. USA* 83:8258-8262, 1986; U.S. Patent No. 4,935,233 and U.S. Patent No. 4,751,180. The linker sequence may be from 1 to about 50 amino acids in length. Peptide sequences are not required when the first and second polypeptides have non-essential N-terminal amino acid regions that can be used to separate the functional domains and prevent steric interference.

The ligated DNA sequences are operably linked to suitable transcriptional or translational regulatory elements. The regulatory elements responsible for expression of DNA are located only 5' to the DNA sequence encoding the first polypeptides. Similarly, stop codons require to end translation and transcription termination signals are only present 3' to the DNA sequence encoding the second polypeptide.

Polypeptides and/or fusion proteins of the present invention may be used to generate binding agents, such as antibodies or fragments thereof, that are capable of detecting metastatic human prostate tumors. Binding agents of the present invention may generally be prepared using methods known to those of ordinary skill in the art, including the representative procedures described herein. Binding agents are capable of differentiating between patients with and without prostate cancer, using the representative assays described

herein. In other words, antibodies or other binding agents raised against a prostate tumor protein, or a suitable portion thereof, will generate a signal indicating the presence of primary or metastatic prostate cancer in at least about 20% of patients afflicted with the disease, and will generate a negative signal indicating the absence of the disease in at least about 90% of individuals without primary or metastatic prostate cancer. Suitable portions of such prostate tumor proteins are portions that are able to generate a binding agent that indicates the presence of primary or metastatic prostate cancer in substantially all (*i.e.*, at least about 80%, and preferably at least about 90%) of the patients for which prostate cancer would be indicated using the full length protein, and that indicate the absence of prostate cancer in substantially all of those samples that would be negative when tested with full length protein. The representative assays described below, such as the two-antibody sandwich assay, may generally be employed for evaluating the ability of a binding agent to detect metastatic human prostate tumors.

The ability of a polypeptide and/or fusion protein prepared as described herein to generate antibodies capable of detecting primary or metastatic human prostate tumors may generally be evaluated by raising one or more antibodies against the polypeptide (using, for example, a representative method described herein) and determining the ability of such antibodies to detect such tumors in patients. This determination may be made by assaying biological samples from patients with and without primary or metastatic prostate cancer for the presence of a polypeptide that binds to the generated antibodies. Such test assays may be performed, for example, using a representative procedure described below. Polypeptides that generate antibodies capable of detecting at least 20% of primary or metastatic prostate tumors by such procedures are considered to be useful in assays for detecting primary or metastatic human prostate tumors. Polypeptide specific antibodies may be used alone or in combination to improve sensitivity.

Polypeptides and/or fusion proteins capable of detecting primary or metastatic human prostate tumors may be used as markers for diagnosing prostate cancer or for monitoring disease progression in patients. In one embodiment, prostate cancer in a patient may be diagnosed by evaluating a biological sample obtained from the patient for the level of

one or more of the above polypeptides, relative to a predetermined cut-off value. As used herein, suitable "biological samples" include blood, sera, urine and/or prostate secretions.

The level of one or more of the above polypeptides may be evaluated using any binding agent specific for the polypeptide(s). A "binding agent," in the context of this invention, is any agent (such as a compound or a cell) that binds to a polypeptide as described above. As used herein, "binding" refers to a noncovalent association between two separate molecules (each of which may be free (*i.e.*, in solution) or present on the surface of a cell or a solid support), such that a "complex" is formed. Such a complex may be free or immobilized (either covalently or noncovalently) on a support material. The ability to bind may generally be evaluated by determining a binding constant for the formation of the complex. The binding constant is the value obtained when the concentration of the complex is divided by the product of the component concentrations. In general, two compounds are said to "bind" in the context of the present invention when the binding constant for complex formation exceeds about 10^3 L/mol. The binding constant may be determined using methods well known to those of ordinary skill in the art.

Any agent that satisfies the above requirements may be a binding agent. For example, a binding agent may be a ribosome with or without a peptide component, an RNA molecule or a peptide. In a preferred embodiment, the binding partner is an antibody, or a fragment thereof. Such antibodies may be polyclonal, or monoclonal. In addition, the antibodies may be single chain, chimeric, CDR-grafted or humanized. Antibodies may be prepared by the methods described herein and by other methods well known to those of skill in the art.

There are a variety of assay formats known to those of ordinary skill in the art for using a binding partner to detect polypeptide markers in a sample. *See, e.g.*, Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In a preferred embodiment, the assay involves the use of binding partner immobilized on a solid support to bind to and remove the polypeptide from the remainder of the sample. The bound polypeptide may then be detected using a second binding partner that contains a reporter group. Suitable second binding partners include antibodies that bind to the binding partner/polypeptide complex. Alternatively, a competitive assay may be utilized, in which a

polypeptide is labeled with a reporter group and allowed to bind to the immobilized binding partner after incubation of the binding partner with the sample. The extent to which components of the sample inhibit the binding of the labeled polypeptide to the binding partner is indicative of the reactivity of the sample with the immobilized binding partner.

The solid support may be any material known to those of ordinary skill in the art to which the antigen may be attached. For example, the solid support may be a test well in a microtiter plate or a nitrocellulose or other suitable membrane. Alternatively, the support may be a bead or disc, such as glass, fiberglass, latex or a plastic material such as polystyrene or polyvinylchloride. The support may also be a magnetic particle or a fiber optic sensor, such as those disclosed, for example, in U.S. Patent No. 5,359,681. The binding agent may be immobilized on the solid support using a variety of techniques known to those of skill in the art, which are amply described in the patent and scientific literature. In the context of the present invention, the term "immobilization" refers to both noncovalent association, such as adsorption, and covalent attachment (which may be a direct linkage between the antigen and functional groups on the support or may be a linkage by way of a cross-linking agent). Immobilization by adsorption to a well in a microtiter plate or to a membrane is preferred. In such cases, adsorption may be achieved by contacting the binding agent, in a suitable buffer, with the solid support for a suitable amount of time. The contact time varies with temperature, but is typically between about 1 hour and about 1 day. In general, contacting a well of a plastic microtiter plate (such as polystyrene or polyvinylchloride) with an amount of binding agent ranging from about 10 ng to about 10 μ g, and preferably about 100 ng to about 1 μ g, is sufficient to immobilize an adequate amount of binding agent.

Covalent attachment of binding agent to a solid support may generally be achieved by first reacting the support with a bifunctional reagent that will react with both the support and a functional group, such as a hydroxyl or amino group, on the binding agent. For example, the binding agent may be covalently attached to supports having an appropriate polymer coating using benzoquinone or by condensation of an aldehyde group on the support with an amine and an active hydrogen on the binding partner (*see, e.g.*, Pierce Immunotechnology Catalog and Handbook, 1991, at A12-A13).

In certain embodiments, the assay is a two-antibody sandwich assay. This assay may be performed by first contacting an antibody that has been immobilized on a solid support, commonly the well of a microtiter plate, with the sample, such that polypeptides within the sample are allowed to bind to the immobilized antibody. Unbound sample is then removed from the immobilized polypeptide-antibody complexes and a second antibody (containing a reporter group) capable of binding to a different site on the polypeptide is added. The amount of second antibody that remains bound to the solid support is then determined using a method appropriate for the specific reporter group.

More specifically, once the antibody is immobilized on the support as described above, the remaining protein binding sites on the support are typically blocked. Any suitable blocking agent known to those of ordinary skill in the art, such as bovine serum albumin or Tween 20™ (Sigma Chemical Co., St. Louis, MO). The immobilized antibody is then incubated with the sample, and polypeptide is allowed to bind to the antibody. The sample may be diluted with a suitable diluent, such as phosphate-buffered saline (PBS) prior to incubation. In general, an appropriate contact time (*i.e.*, incubation time) is that period of time that is sufficient to detect the presence of polypeptide within a sample obtained from an individual with prostate cancer. Preferably, the contact time is sufficient to achieve a level of binding that is at least about 95% of that achieved at equilibrium between bound and unbound polypeptide. Those of ordinary skill in the art will recognize that the time necessary to achieve equilibrium may be readily determined by assaying the level of binding that occurs over a period of time. At room temperature, an incubation time of about 30 minutes is generally sufficient.

Unbound sample may then be removed by washing the solid support with an appropriate buffer, such as PBS containing 0.1% Tween 20™. The second antibody, which contains a reporter group, may then be added to the solid support. Preferred reporter groups include enzymes (such as horseradish peroxidase), substrates, cofactors, inhibitors, dyes, radionuclides, luminescent groups, fluorescent groups and biotin. The conjugation of antibody to reporter group may be achieved using standard methods known to those of ordinary skill in the art.

The second antibody is then incubated with the immobilized antibody-polypeptide complex for an amount of time sufficient to detect the bound polypeptide. An appropriate amount of time may generally be determined by assaying the level of binding that occurs over a period of time. Unbound second antibody is then removed and bound second antibody is detected using the reporter group. The method employed for detecting the reporter group depends upon the nature of the reporter group. For radioactive groups, scintillation counting or autoradiographic methods are generally appropriate. Spectroscopic methods may be used to detect dyes, luminescent groups and fluorescent groups. Biotin may be detected using avidin, coupled to a different reporter group (commonly a radioactive or fluorescent group or an enzyme). Enzyme reporter groups may generally be detected by the addition of substrate (generally for a specific period of time), followed by spectroscopic or other analysis of the reaction products.

To determine the presence or absence of prostate cancer, the signal detected from the reporter group that remains bound to the solid support is generally compared to a signal that corresponds to a predetermined cut-off value. In one preferred embodiment, the cut-off value is the average mean signal obtained when the immobilized antibody is incubated with samples from patients without prostate cancer. In general, a sample generating a signal that is three standard deviations above the predetermined cut-off value is considered positive for prostate cancer. In an alternate preferred embodiment, the cut-off value is determined using a Receiver Operator Curve, according to the method of Sackett et al., *Clinical Epidemiology: A Basic Science for Clinical Medicine*, Little Brown and Co., 1985, p. 106-7. Briefly, in this embodiment, the cut-off value may be determined from a plot of pairs of true positive rates (*i.e.*, sensitivity) and false positive rates (100%-specificity) that correspond to each possible cut-off value for the diagnostic test result. The cut-off value on the plot that is the closest to the upper left-hand corner (*i.e.*, the value that encloses the largest area) is the most accurate cut-off value, and a sample generating a signal that is higher than the cut-off value determined by this method may be considered positive. Alternatively, the cut-off value may be shifted to the left along the plot, to minimize the false positive rate, or to the right, to minimize the false negative rate. In general, a sample generating a signal that is higher than the cut-off value determined by this method is considered positive for prostate cancer.

In a related embodiment, the assay is performed in a flow-through or strip test format, wherein the antibody is immobilized on a membrane, such as nitrocellulose. In the flow-through test, polypeptides within the sample bind to the immobilized antibody as the sample passes through the membrane. A second, labeled antibody then binds to the antibody-polypeptide complex as a solution containing the second antibody flows through the membrane. The detection of bound second antibody may then be performed as described above. In the strip test format, one end of the membrane to which antibody is bound is immersed in a solution containing the sample. The sample migrates along the membrane through a region containing second antibody and to the area of immobilized antibody. Concentration of second antibody at the area of immobilized antibody indicates the presence of prostate cancer. Typically, the concentration of second antibody at that site generates a pattern, such as a line, that can be read visually. The absence of such a pattern indicates a negative result. In general, the amount of antibody immobilized on the membrane is selected to generate a visually discernible pattern when the biological sample contains a level of polypeptide that would be sufficient to generate a positive signal in the two-antibody sandwich assay, in the format discussed above. Preferably, the amount of antibody immobilized on the membrane ranges from about 25 ng to about 1 μ g, and more preferably from about 50 ng to about 500 ng. Such tests can typically be performed with a very small amount of biological sample.

Of course, numerous other assay protocols exist that are suitable for use with the antigens or antibodies of the present invention. The above descriptions are intended to be exemplary only.

In another embodiment, the above polypeptides may be used as markers for the progression of prostate cancer. In this embodiment, assays as described above for the diagnosis of prostate cancer may be performed over time, and the change in the level of reactive polypeptide(s) evaluated. For example, the assays may be performed every 24-72 hours for a period of 6 months to 1 year, and thereafter performed as needed. In general, prostate cancer is progressing in those patients in whom the level of polypeptide detected by the binding agent increases over time. In contrast, prostate cancer is not progressing when the level of reactive polypeptide either remains constant or decreases with time.

Antibodies for use in the above methods may be prepared by any of a variety of techniques known to those of ordinary skill in the art. See, e.g., Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In one such technique, an immunogen comprising the antigenic polypeptide is initially injected into any of a wide variety of mammals (e.g., mice, rats, rabbits, sheep and goats). In this step, the polypeptides of this invention may serve as the immunogen without modification. Alternatively, particularly for relatively short polypeptides, a superior immune response may be elicited if the polypeptide is joined to a carrier protein, such as bovine serum albumin or keyhole limpet hemocyanin. The immunogen is injected into the animal host, preferably according to a predetermined schedule incorporating one or more booster immunizations, and the animals are bled periodically. Polyclonal antibodies specific for the polypeptide may then be purified from such antisera by, for example, affinity chromatography using the polypeptide coupled to a suitable solid support.

Monoclonal antibodies specific for the antigenic polypeptide of interest may be prepared, for example, using the technique of Kohler and Milstein, *Eur. J. Immunol.* 6:511-519, 1976, and improvements thereto. Briefly, these methods involve the preparation of immortal cell lines capable of producing antibodies having the desired specificity (i.e., reactivity with the polypeptide of interest). Such cell lines may be produced, for example, from spleen cells obtained from an animal immunized as described above. The spleen cells are then immortalized by, for example, fusion with a myeloma cell fusion partner, preferably one that is syngeneic with the immunized animal. A variety of fusion techniques may be employed. For example, the spleen cells and myeloma cells may be combined with a nonionic detergent for a few minutes and then plated at low density on a selective medium that supports the growth of hybrid cells, but not myeloma cells. A preferred selection technique uses HAT (hypoxanthine, aminopterin, thymidine) selection. After a sufficient time, usually about 1 to 2 weeks, colonies of hybrids are observed. Single colonies are selected and tested for binding activity against the polypeptide. Hybridomas having high reactivity and specificity are preferred.

Monoclonal antibodies may be isolated from the supernatants of growing hybridoma colonies. In addition, various techniques may be employed to enhance the yield,

such as injection of the hybridoma cell line into the peritoneal cavity of a suitable vertebrate host, such as a mouse. Monoclonal antibodies may then be harvested from the ascites fluid or the blood. Contaminants may be removed from the antibodies by conventional techniques, such as chromatography, gel filtration, precipitation, and extraction. The polypeptides of this invention may be used in the purification process in, for example, an affinity chromatography step.

Monoclonal antibodies of the present invention may also be used as therapeutic reagents, to diminish or eliminate prostate tumors. The antibodies may be used on their own (for instance, to inhibit metastases) or coupled to one or more therapeutic agents. Suitable agents in this regard include radionuclides, differentiation inducers, drugs, toxins, and derivatives thereof. Preferred radionuclides include ^{90}Y , ^{123}I , ^{125}I , ^{131}I , ^{186}Re , ^{188}Re , ^{211}At , and ^{212}Bi . Preferred drugs include methotrexate, and pyrimidine and purine analogs. Preferred differentiation inducers include phorbol esters and butyric acid. Preferred toxins include ricin, abrin, diphtheria toxin, cholera toxin, gelonin, *Pseudomonas* exotoxin, *Shigella* toxin, and pokeweed antiviral protein.

A therapeutic agent may be coupled (*e.g.*, covalently bonded) to a suitable monoclonal antibody either directly or indirectly (*e.g.*, via a linker group). A direct reaction between an agent and an antibody is possible when each possesses a substituent capable of reacting with the other. For example, a nucleophilic group, such as an amino or sulfhydryl group, on one may be capable of reacting with a carbonyl-containing group, such as an anhydride or an acid halide, or with an alkyl group containing a good leaving group (*e.g.*, a halide) on the other.

Alternatively, it may be desirable to couple a therapeutic agent and an antibody via a linker group. A linker group can function as a spacer to distance an antibody from an agent in order to avoid interference with binding capabilities. A linker group can also serve to increase the chemical reactivity of a substituent on an agent or an antibody, and thus increase the coupling efficiency. An increase in chemical reactivity may also facilitate the use of agents, or functional groups on agents, which otherwise would not be possible.

It will be evident to those skilled in the art that a variety of bifunctional or polyfunctional reagents, both homo- and hetero-functional (such as those described in the

catalog of the Pierce Chemical Co., Rockford, IL), may be employed as the linker group. Coupling may be effected, for example, through amino groups, carboxyl groups, sulfhydryl groups or oxidized carbohydrate residues. There are numerous references describing such methodology, *e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.

Where a therapeutic agent is more potent when free from the antibody portion of the immunoconjugates of the present invention, it may be desirable to use a linker group which is cleavable during or upon internalization into a cell. A number of different cleavable linker groups have been described. The mechanisms for the intracellular release of an agent from these linker groups include cleavage by reduction of a disulfide bond (*e.g.*, U.S. Patent No. 4,489,710, to Spitler), by irradiation of a photolabile bond (*e.g.*, U.S. Patent No. 4,625,014, to Senter et al.), by hydrolysis of derivatized amino acid side chains (*e.g.*, U.S. Patent No. 4,638,045, to Kohn et al.), by serum complement-mediated hydrolysis (*e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.), and acid-catalyzed hydrolysis (*e.g.*, U.S. Patent No. 4,569,789, to Blattler et al.).

It may be desirable to couple more than one agent to an antibody. In one embodiment, multiple molecules of an agent are coupled to one antibody molecule. In another embodiment, more than one type of agent may be coupled to one antibody. Regardless of the particular embodiment, immunoconjugates with more than one agent may be prepared in a variety of ways. For example, more than one agent may be coupled directly to an antibody molecule, or linkers which provide multiple sites for attachment can be used. Alternatively, a carrier can be used.

A carrier may bear the agents in a variety of ways, including covalent bonding either directly or via a linker group. Suitable carriers include proteins such as albumins (*e.g.*, U.S. Patent No. 4,507,234, to Kato et al.), peptides and polysaccharides such as aminodextran (*e.g.*, U.S. Patent No. 4,699,784, to Shih et al.). A carrier may also bear an agent by noncovalent bonding or by encapsulation, such as within a liposome vesicle (*e.g.*, U.S. Patent Nos. 4,429,008 and 4,873,088). Carriers specific for radionuclide agents include radiohalogenated small molecules and chelating compounds. For example, U.S. Patent No. 4,735,792 discloses representative radiohalogenated small molecules and their synthesis. A radionuclide chelate may be formed from chelating compounds that include those containing

nitrogen and sulfur atoms as the donor atoms for binding the metal, or metal oxide, radionuclide. For example, U.S. Patent No. 4,673,562, to Davison et al. discloses representative chelating compounds and their synthesis.

A variety of routes of administration for the antibodies and immunoconjugates may be used. Typically, administration will be intravenous, intramuscular, subcutaneous or in the bed of a resected tumor. It will be evident that the precise dose of the antibody/immunoconjugate will vary depending upon the antibody used, the antigen density on the tumor, and the rate of clearance of the antibody.

Diagnostic reagents of the present invention may also comprise DNA sequences encoding one or more of the above polypeptides, or one or more portions thereof. For example, at least two oligonucleotide primers may be employed in a polymerase chain reaction (PCR) based assay to amplify prostate tumor-specific cDNA derived from a biological sample, wherein at least one of the oligonucleotide primers is specific for a DNA molecule encoding a prostate tumor protein of the present invention. The presence of the amplified cDNA is then detected using techniques well known in the art, such as gel electrophoresis. Similarly, oligonucleotide probes specific for a DNA molecule encoding a prostate tumor protein of the present invention may be used in a hybridization assay to detect the presence of an inventive polypeptide in a biological sample.

As used herein, the term "oligonucleotide primer/probe specific for a DNA molecule" means an oligonucleotide sequence that has at least about 80%, preferably at least about 90% and more preferably at least about 95%, identity to the DNA molecule in question. Oligonucleotide primers and/or probes which may be usefully employed in the inventive diagnostic methods preferably have at least about 10-40 nucleotides. In a preferred embodiment, the oligonucleotide primers comprise at least about 10 contiguous nucleotides of a DNA molecule having a sequence selected from SEQ ID Nos: 1-107, 109-111, 115-171, 173-175, 177 and 179-224. Preferably, oligonucleotide probes for use in the inventive diagnostic methods comprise at least about 15 contiguous oligonucleotides of a DNA molecule having a sequence provided in SEQ ID Nos: 1-107, 109-111, 115-171, 173-175, 177 and 179-224. Techniques for both PCR based assays and hybridization assays are well known in the art (see, for example, Mullis et al. *Ibid*; Ehrlich, *Ibid*). Primers or probes may

thus be used to detect prostate tumor-specific sequences in biological samples, including blood, semen, prostate tissue and/or prostate tumor tissue.

Polypeptides of the present invention that comprise an immunogenic portion of a prostate tumor protein may also be used for immunotherapy of prostate cancer, wherein the polypeptide stimulates the patient's own immune response to prostate tumor cells. In further aspects, the present invention provides methods for using one or more of the immunoreactive polypeptides encoded by a DNA molecule having a sequence provided in SEQ ID NO: 1-107, 109-111, 115-171, 173-175, 177 and 179-224 (or DNA encoding such polypeptides) for immunotherapy of prostate cancer in a patient. As used herein, a "patient" refers to any warm-blooded animal, preferably a human. A patient may be afflicted with a disease, or may be free of detectable disease. Accordingly, the above immunoreactive polypeptides may be used to treat prostate cancer or to inhibit the development of prostate cancer. The polypeptides may be administered either prior to or following surgical removal of primary tumors and/or treatment by administration of radiotherapy and conventional chemotherapeutic drugs.

In these aspects, the polypeptide is generally present within a pharmaceutical composition and/or a vaccine. Pharmaceutical compositions may comprise one or more polypeptides, each of which may contain one or more of the above sequences (or variants thereof), and a physiologically acceptable carrier. The vaccines may comprise one or more of such polypeptides and a non-specific immune response enhancer, such as an adjuvant, biodegradable microsphere (e.g., polylactic galactide) or a liposome (into which the polypeptide is incorporated). Pharmaceutical compositions and vaccines may also contain other epitopes of prostate tumor antigens, either incorporated into a combination polypeptide (i.e., a single polypeptide that contains multiple epitopes) or present within a separate polypeptide.

Alternatively, a pharmaceutical composition or vaccine may contain DNA encoding one or more of the above polypeptides, such that the polypeptide is generated *in situ*. In such pharmaceutical compositions and vaccines, the DNA may be present within any of a variety of delivery systems known to those of ordinary skill in the art, including nucleic acid expression systems, bacteria and viral expression systems. Appropriate nucleic acid

expression systems contain the necessary DNA sequences for expression in the patient (such as a suitable promoter). Bacterial delivery systems involve the administration of a bacterium (such as *Bacillus-Calmette-Guerrin*) that expresses an epitope of a prostate cell antigen on its cell surface. In a preferred embodiment, the DNA may be introduced using a viral expression system (e.g., vaccinia or other pox virus, retrovirus, or adenovirus), which may involve the use of a non-pathogenic (defective), replication competent virus. Suitable systems are disclosed, for example, in Fisher-Hoch et al., *PNAS* 86:317-321, 1989; Flexner et al., *Ann. N.Y. Acad. Sci.* 569:86-103, 1989; Flexner et al., *Vaccine* 8:17-21, 1990; U.S. Patent Nos. 4,603,112, 4,769,330, and 5,017,487; WO 89/01973; U.S. Patent No. 4,777,127; GB 2,200,651; EP 0,345,242; WO 91/02805; Berkner, *Biotechniques* 6:616-627, 1988; Rosenfeld et al., *Science* 252:431-434, 1991; Kolls et al., *PNAS* 91:215-219, 1994; Kass-Eisler et al., *PNAS* 90:11498-11502, 1993; Guzman et al., *Circulation* 88:2838-2848, 1993; and Guzman et al., *Cir. Res.* 73:1202-1207, 1993. Techniques for incorporating DNA into such expression systems are well known to those of ordinary skill in the art. The DNA may also be "naked," as described, for example, in published PCT application WO 90/11092, and Ulmer et al., *Science* 259:1745-1749, 1993, reviewed by Cohen, *Science* 259:1691-1692, 1993. The uptake of naked DNA may be increased by coating the DNA onto biodegradable beads, which are efficiently transported into the cells.

Routes and frequency of administration, as well as dosage, will vary from individual to individual and may parallel those currently being used in immunotherapy of other diseases. In general, the pharmaceutical compositions and vaccines may be administered by injection (e.g., intracutaneous, intramuscular, intravenous or subcutaneous), intranasally (e.g., by aspiration) or orally. Between 1 and 10 doses may be administered over a 3-24 week period. Preferably, 4 doses are administered, at an interval of 3 months, and booster administrations may be given periodically thereafter. Alternate protocols may be appropriate for individual patients. A suitable dose is an amount of polypeptide or DNA that is effective to raise an immune response (cellular and/or humoral) against prostate tumor cells in a treated patient. A suitable immune response is at least 10-50% above the basal (i.e., untreated) level. In general, the amount of polypeptide present in a dose (or produced *in situ* by the DNA in a dose) ranges from about 1 pg to about 100 mg per kg of host, typically from

about 10 pg to about 1 mg, and preferably from about 100 pg to about 1 μ g. Suitable dose sizes will vary with the size of the patient, but will typically range from about 0.01 mL to about 5 mL.

While any suitable carrier known to those of ordinary skill in the art may be employed in the pharmaceutical compositions of this invention, the type of carrier will vary depending on the mode of administration. For parenteral administration, such as subcutaneous injection, the carrier preferably comprises water, saline, alcohol, a lipid, a wax and/or a buffer. For oral administration, any of the above carriers or a solid carrier, such as mannitol, lactose, starch, magnesium stearate, sodium saccharine, talcum, cellulose, glucose, sucrose, and/or magnesium carbonate, may be employed. Biodegradable microspheres (e.g., polylactic glycolide) may also be employed as carriers for the pharmaceutical compositions of this invention. Suitable biodegradable microspheres are disclosed, for example, in U.S. Patent Nos. 4,897,268 and 5,075,109.

Any of a variety of non-specific immune response enhancers may be employed in the vaccines of this invention. For example, an adjuvant may be included. Most adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a nonspecific stimulator of immune response, such as lipid A, *Bordella pertussis* or *Mycobacterium tuberculosis*. Such adjuvants are commercially available as, for example, Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI) and Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ).

Polypeptides disclosed herein may also be employed in *ex vivo* treatment of prostate cancer. For example, cells of the immune system, such as T cells, may be isolated from the peripheral blood of a patient, using a commercially available cell separation system, such as CellPro Incorporated's (Bothell, WA) CEPRATE™ system (see U.S. Patent No. 5,240,856; U.S. Patent No. 5,215,926; WO 89/06280; WO 91/16116 and WO 92/07243). The separated cells are stimulated with one or more of the immunoreactive polypeptides contained within a delivery vehicle, such as a microsphere, to provide antigen-specific T cells. The population of tumor antigen-specific T cells is then expanded using standard techniques and the cells are administered back to the patient.

The following Examples are offered by way of illustration and not by way of limitation.

EXAMPLES

EXAMPLE 1

ISOLATION AND CHARACTERIZATION OF PROSTATE TUMOR POLYPEPTIDES

This Example describes the isolation of prostate tumor polypeptides from a prostate tumor cDNA library.

A human prostate tumor cDNA expression library was constructed from prostate tumor poly A⁺ RNA using a Superscript Plasmid System for cDNA Synthesis and Plasmid Cloning kit (BRL Life Technologies, Gaithersburg, MD 20897) following the manufacturer's protocol. Specifically, prostate tumor tissues were homogenized with polytron (Kinematica, Switzerland) and total RNA was extracted using Trizol reagent (BRL Life Technologies) as directed by the manufacturer. The poly A⁺ RNA was then purified using a Qiagen oligotex spin column mRNA purification kit (Qiagen, Santa Clarita, CA 91355) according to the manufacturer's protocol. First-strand cDNA was synthesized using the NotI/Oligo-dT18 primer. Double-stranded cDNA was synthesized, ligated with EcoRI/BAXI adaptors (Invitrogen, San Diego, CA) and digested with NotI. Following size fractionation with Chroma Spin-1000 columns (Clontech, Palo Alto, CA 94303), the cDNA was ligated into the EcoRI/NotI site of pCDNA3.1 (Invitrogen) and transformed into ElectroMax *E. coli* DH10B cells (BRL Life Technologies) by electroporation.

Using the same procedure, a normal human pancreas cDNA expression library was prepared from a pool of six tissue specimens (Clontech). The cDNA libraries were characterized by determining the number of independent colonies, the percentage of clones that carried insert, the average insert size and by sequence analysis. The prostate tumor library contained 1.64×10^7 independent colonies, with 70% of clones having an insert and the average insert size being 1745 base pairs. The normal pancreas cDNA library contained 3.3×10^6 independent colonies, with 69% of clones having inserts and the average insert size

being 1120 base pairs. For both libraries, sequence analysis showed that the majority of clones had a full length cDNA sequence and were synthesized from mRNA, with minimal rRNA and mitochondrial DNA contamination.

cDNA library subtraction was performed using the above prostate tumor and normal pancreas cDNA libraries, as described by Hara et al. (*Blood*, 84:189-199, 1994) with some modifications. Specifically, a prostate tumor-specific subtracted cDNA library was generated as follows. Normal pancreas cDNA library (70 µg) was digested with EcoRI, NotI, and SfuI, followed by a filling-in reaction with DNA polymerase Klenow fragment. After phenol-chloroform extraction and ethanol precipitation, the DNA was dissolved in 100 µl of H₂O, heat-denatured and mixed with 100 µl (100 µg) of Photoprobe biotin (Vector Laboratories, Burlingame, CA). As recommended by the manufacturer, the resulting mixture was irradiated with a 270 W sunlamp on ice for 20 minutes. Additional Photoprobe biotin (50 µl) was added and the biotinylation reaction was repeated. After extraction with butanol five times, the DNA was ethanol-precipitated and dissolved in 23 µl H₂O to form the driver DNA.

To form the tracer DNA, 10 µg prostate tumor cDNA library was digested with BamHI and XhoI, phenol chloroform extracted and passed through Chroma spin-400 columns (Clontech). Following ethanol precipitation, the tracer DNA was dissolved in 5 µl H₂O. Tracer DNA was mixed with 15 µl driver DNA and 20 µl of 2 x hybridization buffer (1.5 M NaCl/10 mM EDTA/50 mM HEPES pH 7.5/0.2% sodium dodecyl sulfate), overlaid with mineral oil, and heat-denatured completely. The sample was immediately transferred into a 68 °C water bath and incubated for 20 hours (long hybridization [LH]). The reaction mixture was then subjected to a streptavidin treatment followed by phenol/chloroform extraction. This process was repeated three more times. Subtracted DNA was precipitated, dissolved in 12 µl H₂O, mixed with 8 µl driver DNA and 20 µl of 2 x hybridization buffer, and subjected to a hybridization at 68 °C for 2 hours (short hybridization [SH]). After removal of biotinylated double-stranded DNA, subtracted cDNA was ligated into BamHI/XhoI site of chloramphenicol resistant pBCSK⁺ (Stratagene, La Jolla, CA 92037) and transformed into ElectroMax *E. coli* DH10B cells by electroporation to generate a prostate tumor specific subtracted cDNA library (prostate subtraction 1).

To analyze the subtracted cDNA library, plasmid DNA was prepared from 100 independent clones, randomly picked from the subtracted prostate tumor specific library and grouped based on insert size. Representative cDNA clones were further characterized by DNA sequencing with a Perkin Elmer/Applied Biosystems Division Automated Sequencer Model 373A (Foster City, CA). Six cDNA clones, hereinafter referred to as F1-13, F1-12, F1-16, H1-1, H1-9 and H1-4, were shown to be abundant in the subtracted prostate-specific cDNA library. The determined 3' and 5' cDNA sequences for F1-12 are provided in SEQ ID NO: 2 and 3, respectively, with determined 3' cDNA sequences for F1-13, F1-16, H1-1, H1-9 and H1-4 being provided in SEQ ID No: 1 and 4-7, respectively.

The cDNA sequences for the isolated clones were compared to known sequences in the gene bank using the EMBL and GenBank databases (release 96). Four of the prostate tumor cDNA clones, F1-13, F1-16, H1-1, and H1-4, were determined to encode the following previously identified proteins: prostate specific antigen (PSA), human glandular kallikrein, human tumor expression enhanced gene, and mitochondria cytochrome C oxidase subunit II. H1-9 was found to be identical to a previously identified human autonomously replicating sequence. No significant homologies to the cDNA sequence for F1-12 were found.

Subsequent studies led to the isolation of a full-length cDNA sequence for F1-12. This sequence is provided in SEQ ID NO: 107, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 108.

To clone less abundant prostate tumor specific genes, cDNA library subtraction was performed by subtracting the prostate tumor cDNA library described above with the normal pancreas cDNA library and with the three most abundant genes in the previously subtracted prostate tumor specific cDNA library: human glandular kallikrein, prostate specific antigen (PSA), and mitochondria cytochrome C oxidase subunit II. Specifically, 1 µg each of human glandular kallikrein, PSA and mitochondria cytochrome C oxidase subunit II cDNAs in pCDNA3.1 were added to the driver DNA and subtraction was performed as described above to provide a second subtracted cDNA library hereinafter referred to as the "subtracted prostate tumor specific cDNA library with spike".

Twenty-two cDNA clones were isolated from the subtracted prostate tumor specific cDNA library with spike. The determined 3' and 5' cDNA sequences for the clones referred to as J1-17, L1-12, N1-1862, J1-13, J1-19, J1-25, J1-24, K1-58, K1-63, L1-4 and L1-14 are provided in SEQ ID Nos: 8-9, 10-11, 12-13, 14-15, 16-17, 18-19, 20-21, 22-23, 24-25, 26-27 and 28-29, respectively. The determined 3' cDNA sequences for the clones referred to as J1-12, J1-16, J1-21, K1-48, K1-55, L1-2, L1-6, N1-1858, N1-1860, N1-1861, N1-1864 are provided in SEQ ID Nos: 30-40, respectively. Comparison of these sequences with those in the gene bank as described above, revealed no significant homologies to three of the five most abundant DNA species, (J1-17, L1-12 and N1-1862; SEQ ID Nos: 8-9, 10-11 and 12-13, respectively). Of the remaining two most abundant species, one (J1-12; SEQ ID NO:30) was found to be identical to the previously identified human pulmonary surfactant-associated protein, and the other (K1-48; SEQ ID NO:33) was determined to have some homology to *R. norvegicus* mRNA for 2-arylpropionyl-CoA epimerase. Of the 17 less abundant cDNA clones isolated from the subtracted prostate tumor specific cDNA library with spike, four (J1-16, K1-55, L1-6 and N1-1864; SEQ ID Nos:31, 34, 36 and 40, respectively) were found to be identical to previously identified sequences, two (J1-21 and N1-1860; SEQ ID Nos: 32 and 38, respectively) were found to show some homology to non-human sequences, and two (L1-2 and N1-1861; SEQ ID Nos: 35 and 39, respectively) were found to show some homology to known human sequences. No significant homologies were found to the polypeptides J1-13, J1-19, J1-24, J1-25, K1-58, K1-63, L1-4, L1-14 (SEQ ID Nos: 14-15, 16-17, 20-21, 18-19, 22-23, 24-25, 26-27, 28-29, respectively).

Subsequent studies led to the isolation of full length cDNA sequences for J1-17, L1-12 and N1-1862 (SEQ ID NOS: 109-111, respectively). The corresponding predicted amino acid sequences are provided in SEQ ID NOS: 112-114.

In a further experiment, four additional clones were identified by subtracting a prostate tumor cDNA library with normal prostate cDNA prepared from a pool of three normal prostate poly A+ RNA (prostate subtraction 2). The determined cDNA sequences for these clones, hereinafter referred to as U1-3064, U1-3065, V1-3692 and 1A-3905, are provided in SEQ ID NO: 69-72, respectively. Comparison of the determined sequences with those in the gene bank revealed no significant homologies to U1-3065.

A second subtraction with spike (prostate subtraction spike 2) was performed by subtracting a prostate tumor specific cDNA library with spike with normal pancreas cDNA library and further spiked with PSA, J1-17, pulmonary surfactant-associated protein, mitochondrial DNA, cytochrome c oxidase subunit II, N1-1862, autonomously replicating sequence, L1-12 and tumor expression enhanced gene. Four additional clones, hereinafter referred to as V1-3686, R1-2330, 1B-3976 and V1-3679, were isolated. The determined cDNA sequences for these clones are provided in SEQ ID NO:73-76, respectively. Comparison of these sequences with those in the gene bank revealed no significant homologies to V1-3686 and R1-2330.

Further analysis of the three prostate subtractions described above (prostate subtraction 2, subtracted prostate tumor specific cDNA library with spike, and prostate subtraction spike 2) resulted in the identification of sixteen additional clones, referred to as 1G-4736, 1G-4738, 1G-4741, 1G-4744, 1G-4734, 1H-4774, 1H-4781, 1H-4785, 1H-4787, 1H-4796, 1I-4810, 1I-4811, 1J-4876, 1K-4884 and 1K-4896. The determined cDNA sequences for these clones are provided in SEQ ID NOS: 77-92, respectively. Comparison of these sequences with those in the gene bank as described above, revealed no significant homologies to 1G-4741, 1G-4734, 1I-4807, 1J-4876 and 1K-4896 (SEQ ID NOS: 79, 81, 87, 90 and 92, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1G-4736, 1G-4738, 1G-4741, 1G-4744, 1H-4774, 1H-4781, 1H-4785, 1H-4787, 1H-4796, 1I-4807, 1J-4876, 1K-4884 and 1K-4896, provided in SEQ ID NOS: 179-188 and 191-193, respectively, and to the determination of additional partial cDNA sequences for 1I-4810 and 1I-4811, provided in SEQ ID NOS: 189 and 190, respectively.

An additional subtraction was performed by subtracting a normal prostate cDNA library with normal pancreas cDNA (prostate subtraction 3). This led to the identification of six additional clones referred to as 1G-4761, 1G-4762, 1H-4766, 1H-4770, 1H-4771 and 1H-4772 (SEQ ID NOS: 93-98). Comparison of these sequences with those in the gene bank revealed no significant homologies to 1G-4761 and 1H-4771 (SEQ ID NOS: 93 and 97, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1G-4761, 1G-4762, 1H-4766 and 1H-4772 provided in SEQ

ID NOS: 194-196 and 199, respectively, and to the determination of additional partial cDNA sequences for 1H-4770 and 1H-4771, provided in SEQ ID NOS: 197 and 198, respectively.

Subtraction of a prostate tumor cDNA library, prepared from a pool of polyA+ RNA from three prostate cancer patients, with a normal pancreas cDNA library (prostate subtraction 4) led to the identification of eight clones, referred to as 1D-4297, 1D-4309, 1D.1-4278, 1D-4288, 1D-4283, 1D-4304, 1D-4296 and 1D-4280 (SEQ ID NOS: 99-107). These sequences were compared to those in the gene bank as described above. No significant homologies were found to 1D-4283 and 1D-4304 (SEQ ID NOS: 103 and 104, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1D-4309, 1D.1-4278, 1D-4288, 1D-4283, 1D-4304, 1D-4296 and 1D-4280, provided in SEQ ID NOS: 200-206, respectively.

cDNA clones isolated in prostate subtraction 1 and prostate subtraction 2, described above, were colony PCR amplified and their mRNA expression levels in prostate tumor, normal prostate and in various other normal tissues were determined using microarray technology (Synteni, Palo Alto, CA). Briefly, the PCR amplification products were dotted onto slides in an array format, with each product occupying a unique location in the array. mRNA was extracted from the tissue sample to be tested, reverse transcribed, and fluorescent-labeled cDNA probes were generated. The microarrays were probed with the labeled cDNA probes, the slides scanned and fluorescence intensity was measured. This intensity correlates with the hybridization intensity. Two novel clones (referred to as P509S and P510S) were found to be over-expressed in prostate tumor and normal prostate and expressed at low levels in all other normal tissues tested (liver, pancreas, skin, bone marrow, brain, breast, adrenal gland, bladder, testes, salivary gland, large intestine, kidney, ovary, lung, spinal cord, skeletal muscle and colon). The determined cDNA sequences for P509S and P510S are provided in SEQ ID NO: 223 and 224, respectively. Comparison of these sequences with those in the gene bank as described above, revealed some homology to previously identified ESTs.

EXAMPLE 2

DETERMINATION OF TISSUE SPECIFICITY OF PROSTATE TUMOR POLYPEPTIDES

Using gene specific primers, mRNA expression levels for the representative prostate tumor polypeptides F1-16, H1-1, J1-17, L1-12, F1-12 and N1-1862 were examined in a variety of normal and tumor tissues using RT-PCR.

Briefly, total RNA was extracted from a variety of normal and tumor tissues using Trizol reagent as described above. First strand synthesis was carried out using 1-2 μ g of total RNA with SuperScript II reverse transcriptase (BRL Life Technologies) at 42 °C for one hour. The cDNA was then amplified by PCR with gene-specific primers. To ensure the semi-quantitative nature of the RT-PCR, β -actin was used as an internal control for each of the tissues examined. First, serial dilutions of the first strand cDNAs were prepared and RT-PCR assays were performed using β -actin specific primers. A dilution was then chosen that enabled the linear range amplification of the β -actin template and which was sensitive enough to reflect the differences in the initial copy numbers. Using these conditions, the β -actin levels were determined for each reverse transcription reaction from each tissue. DNA contamination was minimized by DNase treatment and by assuring a negative PCR result when using first strand cDNA that was prepared without adding reverse transcriptase.

mRNA Expression levels were examined in four different types of tumor tissue (prostate tumor from 2 patients, breast tumor from 3 patients, colon tumor, lung tumor), and sixteen different normal tissues, including prostate, colon, kidney, liver, lung, ovary, pancreas, skeletal muscle, skin, stomach, testes, bone marrow and brain. F1-16 was found to be expressed at high levels in prostate tumor tissue, colon tumor and normal prostate, and at lower levels in normal liver, skin and testes, with expression being undetectable in the other tissues examined. H1-1 was found to be expressed at high levels in prostate tumor, lung tumor, breast tumor, normal prostate, normal colon and normal brain, at much lower levels in normal lung, pancreas, skeletal muscle, skin, small intestine, bone marrow, and was not detected in the other tissues tested. J1-17 and L1-12 appear to be specifically over-expressed in prostate, with both genes being expressed at high levels in prostate tumor and normal prostate but at low to undetectable levels in all the other tissues

examined. N1-1862 was found to be over-expressed in 60% of prostate tumors and detectable in normal colon and kidney. The RT-PCR results thus indicate that F1-16, H1-1, J1-17, N1-1862 and L1-12 are either prostate specific or are expressed at significantly elevated levels in prostate.

Further RT-PCR studies showed that F1-12 is over-expressed in 60% of prostate tumors, detectable in normal kidney but not detectable in all other tissues tested. Similarly, R1-2330 was shown to be over-expressed in 40% of prostate tumors, detectable in normal kidney and liver, but not detectable in all other tissues tested. U1-3064 was found to be over-expressed in 60% of prostate tumors, and also expressed in breast and colon tumors, but was not detectable in normal tissues.

RT-PCR characterization of R1-2330, U1-3064 and 1D-4279 showed that these three antigens are over-expressed in prostate and/or prostate tumors.

Northern analysis with four prostate tumors, two normal prostate samples, two BPH prostates, and normal colon, kidney, liver, lung, pancreas, skeletal muscle, brain, stomach, testes, small intestine and bone marrow, showed that L1-12 is over-expressed in prostate tumors and normal prostate, while being undetectable in other normal tissues tested. J1-17 was detected in two prostate tumors and not in the other tissues tested. N1-1862 was found to be over-expressed in three prostate tumors and to be expressed in normal prostate, colon and kidney, but not in other tissues tested. F1-12 was found to be highly expressed in two prostate tumors and to be undetectable in all other tissues tested.

The micro-array technology described above was used to determine the expression levels of representative antigens described herein in prostate tumor, breast tumor and the following normal tissues: prostate, liver, pancreas, skin, bone marrow, brain, breast, adrenal gland, bladder, testes, salivary gland, large intestine, kidney, ovary, lung, spinal cord, skeletal muscle and colon. L1-12 was found to be over-expressed in normal prostate and prostate tumor, with some expression being detected in normal skeletal muscle. Both J1-12 and F1-12 were found to be over-expressed in prostate tumor, with expression being lower or undetectable in all other tissues tested. N1-1862 was found to be expressed at high levels in prostate tumor and normal prostate, and at low levels in normal large intestine and normal colon, with expression being undetectable in all other tissues tested. R1-2330 was found to

be over-expressed in prostate tumor and normal prostate, and to be expressed at lower levels in all other tissues tested. 1D-4279 was found to be over-expressed in prostate tumor and normal prostate, expressed at lower levels in normal spinal cord, and to be undetectable in all other tissues tested.

Example 3

ISOLATION AND CHARACTERIZATION OF PROSTATE TUMOR POLYPEPTIDES BY PCR-BASED SUBTRACTON

A cDNA subtraction library, containing cDNA from normal prostate subtracted with ten other normal tissue cDNAs (brain, heart, kidney, liver, lung, ovary, placenta, skeletal muscle, spleen and thymus) and then submitted to a first round of PCR amplification, was purchased from Clontech. This library was subjected to a second round of PCR amplification, following the manufacturer's protocol. The resulting cDNA fragments were subcloned into the vector pT7 Blue T-vector (Novagen, Madison, WI) and transformed into XL-1 Blue MRF' *E. coli* (Stratagene). DNA was isolated from independent clones and sequenced using a Perkin Elmer/Applied Biosystems Division Automated Sequencer Model 373A.

Fifty-nine positive clones were sequenced. Comparison of the DNA sequences of these clones with those in the gene bank, as described above, revealed no significant homologies to 25 of these clones, hereinafter referred to as P5, P8, P9, P18, P20, P30, P34, P36, P38, P39, P42, P49, P50, P53, P55, P60, P64, P65, P73, P75, P76, P79, and P84. The determined cDNA sequences for these clones are provided in SEQ ID NO:41-45, 47-52 and 54-65, respectively. P29, P47, P68, P80 and P82 (SEQ ID NO:46, 53 and 66-68, respectively) were found to show some degree of homology to previously identified DNA sequences. To the best of the inventors' knowledge, none of these sequences have been previously shown to be present in prostate. Further studies using the PCR-based methodology described above resulted in the isolation of more than 180 additional clones, of which 23 clones were found to show no significant

homologies to known sequences. The determined cDNA sequences for these clones are provided in SEQ ID NO: 115-123, 127, 131, 137, 145, 147-151, 153, 156-158 and 160. Twenty-three clones (SEQ ID NO: 124-126, 128-130, 132-136, 138-144, 146, 152, 154, 155 and 159) were found to show some homology to previously identified ESTs. An additional ten clones (SEQ ID NO: 161-170) were found to have some degree of homology to known genes. An additional clone, referred to as P703, was found to have five splice variants. The determined DNA sequence for the variants referred to as DE1, DE13 and DE14 are provided in SEQ ID NOS: 171, 175 and 177, respectively, with the corresponding predicted amino acid sequences being provided in SEQ ID NO: 172, 176 and 178, respectively. The DNA sequences for the splice variants referred to as DE2 and DE6 are provided in SEQ ID NOS: 173 and 174, respectively.

mRNA Expression levels for representative clones in tumor tissues (prostate (n=5), breast (n=2), colon and lung) normal tissues (prostate (n=5), colon, kidney, liver, lung (n=2), ovary (n=2), skeletal muscle, skin, stomach, small intestine and brain), and activated and non-activated PBMC was determined by RT-PCT as described above. Expression was examined in one sample of each tissue type unless otherwise indicated.

P9 was found to be highly expressed in normal prostate and prostate tumor compared to all normal tissues tested except for normal colon which showed comparable expression. P20 was found to be highly expressed in normal prostate and prostate tumor, compared to all twelve normal tissues tested. A modest increase in expression of P20 in breast tumor (n=2), colon tumor and lung tumor was seen compared to all normal tissues except lung (1 of 2). Increased expression of P18 was found in normal prostate, prostate tumor and breast tumor compared to other normal tissues except lung and stomach. A modest increase in expression of P5 was observed in normal prostate compared to most other normal tissues. However, some elevated expression was seen in normal lung and PBMC. Elevated expression of P5 was also observed in prostate tumors (2 of 5), breast tumor and one lung tumor sample. For P30, similar expression levels were seen in normal prostate and prostate tumor, compared to six of twelve other normal tissues tested. Increased expression was seen in breast tumors, one lung tumor sample and one colon tumor sample, and also in normal PBMC. P29 was found to be over-expressed in prostate tumor (5 of 5) and normal prostate (5

of 5) compared to the majority of normal tissues. However, substantial expression of P29 was observed in normal colon and normal lung (2 of 2). P80 was found to be over-expressed in prostate tumor (5 of 5) and normal prostate (5 of 5) compared to all other normal tissues tested, with increased expression also being seen in colon tumor.

Further studies using the above methodology resulted in the isolation of twelve additional clones, hereinafter referred to as 10-d8, 10-h10, 11-c8, 7-g6, 8-b5, 8-b6, 8-d4, 8-d9, 8-g3, 8-h11, g-f12 and g-f3. The determined DNA sequences for 10-d8, 10-h10, 11-c8, 8-d4, 8-d9, 8-h11, g-f12 and g-f3 are provided in SEQ ID NO: 207, 208, 209, 216, 217, 220, 221 and 222, respectively. The determined forward and reverse DNA sequences for 7-g6, 8-b5, 8-b6 and 8-g3 are provided in SEQ ID NO: 210 and 211; 212 and 213; 214 and 215; and 218 and 219, respectively. Comparison of these sequences with those in the gene bank revealed no significant homologies to the sequences of 7-g6 and g-f3. The clones 10-d8, 11-c8 and 8-h11 were found to show some homology to previously isolated ESTs, while 10-h10, 8-b5, 8-b6, 8-d4, 8-d9, 8-g3 and g-f12 were found to show some homology to previously identified genes.

EXAMPLE 4

SYNTHESIS OF POLYPEPTIDES

Polypeptides may be synthesized on an Applied Biosystems 430A peptide synthesizer using Fmoc chemistry with HPTU (O-Benzotriazole-N,N,N',N'-tetramethyluronium hexafluorophosphate) activation. A Gly-Cys-Gly sequence may be attached to the amino terminus of the peptide to provide a method of conjugation, binding to an immobilized surface, or labeling of the peptide. Cleavage of the peptides from the solid support may be carried out using the following cleavage mixture: trifluoroacetic acid:ethanedithiol:thioanisole:water:phenol (40:1:2:2:3). After cleaving for 2 hours, the peptides may be precipitated in cold methyl-t-butyl-ether. The peptide pellets may then be dissolved in water containing 0.1% trifluoroacetic acid (TFA) and lyophilized prior to purification by C18 reverse phase HPLC. A gradient of 0%-60% acetonitrile (containing 0.1% TFA) in water (containing 0.1% TFA) may be used to elute the peptides. Following

lyophilization of the pure fractions, the peptides may be characterized using electrospray or other types of mass spectrometry and by amino acid analysis.

From the foregoing, it will be appreciated that, although specific embodiments of the invention have been described herein for the purposes of illustration, various modifications may be made without deviating from the spirit and scope of the invention.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANTS: Xu, Jiangchun
Dillon, Davin C.
- (ii) TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER
AND METHODS FOR THEIR USE
- (iii) NUMBER OF SEQUENCES: 224
- (iv) CORRESPONDENCE ADDRESS:
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 - (B) STREET: 6300 Columbia Center, 701 Fifth Avenue
 - (C) CITY: Seattle
 - (D) STATE: WA
 - (E) COUNTRY: USA
 - (F) ZIP: 98104
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE: 23-FEB-1998
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Maki, David J.
 - (B) REGISTRATION NUMBER: 31,392
 - (C) REFERENCE/DOCKET NUMBER: 210121.428C3
- (ix) TELECOMMUNICATION INFORMATION:
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 814 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TTTTTTTTTT TTTTCACAG TATAACAGCT CTTTATTCT GTGAGTTCTA CTAGGAAATC

ATCAAATCTG	AGGGTTGTCT	GGAGGACTTC	AATACACCTC	CCCCCATAGT	GAATCAGCTT	120
CCAGGGGGTC	CAGTCCCTCT	CCTTACTTCA	TCCCCATCCC	ATGCCAAAGG	AAGACCCTCC	180
CTCCTTGGCT	CACAGCCTTC	TCTAGGCTTC	CCAGTGCCTC	CAGGACAGAG	TGGGTTATGT	240
TTTCAGCTCC	ATCCTTGCTG	TGAGTGTCTG	GTGCGTTGTG	CCTCCAGCTT	CTGCTCAGTG	300
CTTCATGGAC	AGTGTCCAGC	ACATGTCACT	CTCCACTCTC	TCAGTGTGGA	TCCACTAGTT	360
CTAGAGCGGC	CGCCACCGCG	GTGGAGCTCC	AGCTTTTGTT	CCCTTTAGTG	AGGGTTAATT	420
GCGCGCTTGG	CGTAATCATG	GTCATAACTG	TTTCTGTGTG	GAAATTGTTA	TCCGCTCACA	480
ATTCCACACA	ACATACGAGC	CGGAAGCATA	AAGTGTAAG	CCTGGGGTGC	CTAATGAGTG	540
ANCTAACTCA	CATTAATTGC	GTTGCGCTCA	CTGNCCGCTT	TCCAGTCNGG	AAAACTGTCTG	600
TGCCAGCTGC	ATTAATGAAT	CGGCCAACGC	NCGGGGAAAA	GCGGTTTGCG	TTTGGGGGGC	660
TCTTCCGCTT	CTCGCTCACT	NANTCCTGCG	CTCGGTCNTT	CGGCTGCGGG	GAACGGTATC	720
ACTCCTCAAA	GGNGGTATTA	CGGTTATCCN	NAAATCNGGG	GATACCCNGG	AAAAAANTTT	780
AACAAAAGGG	CANCAAAGGG	CNGAAACGTA	AAAA			814

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ACAGAAATGT	TGGATGGTGG	AGCACCTTTC	TATACGACTT	ACAGGACAGC	AGATGGGGAA	60
TTCATGGCTG	TTGGAGCAAT	AGAACCCAG	TTCTACGAGC	TGCTGATCAA	AGGACTTGGA	120
CTAAAGTCTG	ATGAACCTCC	CAATCAGATG	AGCATGGATG	ATTGGCCAGA	AATGAAGAAG	180
AAGTTTGCAG	ATGTATTTGC	AAAGAAGACG	AAGGCAGAGT	GGTGTCAAAT	CTTTGACGGC	240
ACAGATGCCT	GTGTGACTCC	GGTTCTGACT	TTTGAGGAGG	TTGTTTCATCA	TGATCACAAC	300
AAGGAACGGG	GCTCGTTTAT	CACCAAGTGG	GAGCAGGACG	TGAGCCCCCG	CCCTGCACCT	360
CTGCTGTAA	ACACCCAGC	CATCCCTTCT	TTCAAAAGGG	ATCCACTAGT	TCTAGAAGCG	420
GCCGCCACCG	CGGTGGAGCT	CCAGCTTTTG	TTCCCTTTAG	TGAGGGTTAA	TTGCGCGCTT	480
GGCGTAATCA	TGGTCATAGC	TGTTTCCTGT	GTGAAATTGT	TATCCGCTCA	CAATTCCCCC	540
AACATACGAG	CCGGAACATA	AAGTGTTAAG	CCTGGGGTGC	CTAATGANTG	AGCTAACTCN	600
CATTAATTGC	GTTGCGCTCA	CTGCCCCTT	TCCAGTCGGG	AAAACTGTCTG	TGCCACTGCN	660
TTANTGAATC	NGCCACCCCC	CGGGAAAAGG	CGGTTGCNTT	TTGGGCCTCT	TCCGCTTTCC	720
TCGCTCATTG	ATCCTNGCNC	CCGGTCTTCG	GCTGCGNGA	ACGGTTCACT	CCTCAAAGGC	780
GGTNTNCCGG	TTATCCCCAA	ACNGGGGATA	CCCNCA			816

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 773 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTTTTGAAAG	AAGGGATGGC	TGGGGTGTTT	AACAGCAGAG	GTGCAGGGCG	GGGGCTCACG	60
TCCTGCTCCT	CACTGGTGAT	AAACGAGCCC	CGTTCCTTGT	TGTGATCATG	ATGAACAACC	120

TCCTCAAAAG	TCAGAACCGG	AGTCACACAG	GCATCTGTGC	CGTCAAAGAT	TTGACACCAC	180
TCTGCCTTCG	TCTTCTTTGC	AAATACATCT	GCAAACCTTCT	TCTTCATTTC	TGGCCAATCA	240
TCCATGCTCA	TCTGATTGGG	AAGTTCATCA	GACTTTAGTC	CANNTCCTTT	GATCAGCAGC	300
TCGTAGAACT	GGGGTTCTAT	TGCTCCAACA	GCCATGAATT	CCCCATCTGC	TGTCCTGTAA	360
GTCGTATAGA	AAGGTGCTCC	ACCATCCAAC	ATGTTCTGTC	CTCGAGGGGG	GGCCCGGTAC	420
CCAATTCGCC	CTATANTGAG	TCGTATTACG	CGCGCTCACT	GGCCGTCGTT	TTACAACGTC	480
GTGACTGGGA	AAACCCTGGG	CGTTACCAAC	TTAATCGCCT	TGCAGCACAT	CCCCCTTTTCG	540
CCAGCTGGGC	GTAATANCGA	AAAGGCCCGC	ACCGATCGCC	CTTCCAACAG	TTGCGCACCT	600
GAATGGGNAA	ATGGGACCCC	CCTGTTACCG	CGCATTNAAC	CCCCGCNGGG	TTTNGTTGTT	660
ACCCCCACNT	NNACCGCTTA	CACTTTGCCA	GCGCCTTANC	GCCCCGCTCCC	TTTCNCCTTT	720
CTTCCCTTCC	TTTCNCNCCN	CTTCCCCCGG	GGGTTTCCCC	CNTCAAACCC	CNA	773

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CCTCTGAGT	CCTACTGACC	TGTGCTTTCT	GGTGTGGAGT	CCAGGGCTGC	TAGGAAAAGG	60
AATGGGCAGA	CACAGGTGTA	TGCCAATGTT	TCTGAAATGG	GTATAATTTC	GTCCTCTCCT	120
TCGGAACACT	GGCTGTCTCT	GAAGACTTCT	CGCTCAGTTT	CAGTGAGGAC	ACACACAAAG	180
ACGTGGGTGA	CCATGTTGTT	TGTGGGGTGC	AGAGATGGGA	GGGGTGGGGC	CCACCCTGGA	240
AGAGTGACAC	GTGACACAAG	GTGGACACTC	TCTACAGATC	ACTGAGGATA	AGCTGGAGCC	300
ACAATGCATG	AGGCACACAC	ACAGCAAGGA	TGACNCTGTA	AACATAGCCC	ACGCTGTCCT	360
GNGGGCACTG	GGAAGCCTAN	ATNAGGCCGT	GAGCANAAAG	AAGGGGAGGA	TCCACTAGTT	420
CTANAGCGGC	CGCCACCGCG	GTGGANCTCC	ANCTTTTGTT	CCCTTTAGTG	AGGGTTAATT	480
GCGCGCTTGG	CNTAATCATG	GTGATANCTN	TTTCTGTGTG	GAAATTGTTA	TCCGCTCACA	540
ATTCCACACA	ACATACGANC	CGGAAACATA	AANTGTAAAC	CTGGGGTGCC	TAATGANTGA	600
CTAACTCACA	TTAATTGCGT	TGCGCTCACT	GCCCGCTTTC	CAATCNGGAA	ACCTGTCTTG	660
CCNCTTGAT	TNATGAATCN	GCCAACCCCC	GGGGAAAAGC	GTTTGCGTTT	TGGGCGCTCT	720
TCCGTTTCCT	CNCTCANTTA	NTCCCTNCNC	TCCGTCATTC	CGGCTGCNGC	AAACCGGTTT	780
ACCNCCTCCA	AAGGGGGTAT	TCCGTTTCC	CCNAATCCGG	GGANANCC		828

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TTTTTTTTTT	TTTTTACTGA	TAGATGGAAT	TTATTAAGCT	TTTCACATGT	GATAGCACAT	60
AGTTTTAATT	GCATCCAAAG	TACTAACAAA	AACCTAGCA	ATCAAGAATG	GCAGCATGTT	120
ATTTTATAAC	AATCAACACC	TGTGGCTTTT	AAAATTTGGT	TTTCATAAGA	TAATTTATAC	180
TGAAGTAAAT	CTAGCCATGC	TTTTAAAAAA	TGCTTTAGGT	CACTCCAAGC	TTGGCAGTTA	240

ACATTTGGCA	TAAACAATA	TAAAACAATC	ACAATTTAAT	AAATAACAAA	TACAACATTG	300
TAGGCCATA	TCATATACAG	TATAAGGAAA	AGGTGGTAGT	GTTGAGTAAG	CAGTTATTAG	360
AATAGAATAC	CTTGGCCTCT	ATGCAAATAT	GTCTAGACAC	TTTGATTTCAC	TCAGCCCTGA	420
CATTCACTTT	TCAAAGTAGG	AGACAGGTTC	TACAGTATCA	TTTTACAGTT	TCCAACACAT	480
TGAAAACAAG	TAGAAAATGA	TGAGTTGATT	TTTATTAATG	CATTACATCC	TCAAGAGTTA	540
TCACCAACCC	CTCAGTTATA	AAAAATTTTC	AAGTTATATT	AGTCATATAA	CTTGGTGTGC	600
TTATTTTAAA	TTAGTGCTAA	ATGGATTAAG	TGAAGACAAC	AATGGTCCCC	TAATGTGATT	660
GATATTGGTC	ATTTTTACCA	GCTTCTAAAT	CTNAACTTTC	AGGCTTTTGA	ACTGGAACAT	720
TGNATNACAG	TGTTCCANAG	TTNCAACCTA	CTGGAACATT	ACAGTGTGCT	TGATTCAAAA	780
TGTTATTTTG	TTAAAAATTA	AATTTTAACC	TGGTGGAAAA	ATAATTTGAA	ATNA	834

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 818 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TTTTTTTTTT	TTTTTTTTTT	AAGACCCTCA	TCAATAGATG	GAGACATACA	GAAATAGTCA	60
AACCACATCT	ACAAAATGCC	AGTATCAGGC	GGCGGCTTCG	AAGCCAAAGT	GATGTTTGGA	120
TGTAAAGTGA	AATATTAGTT	GGCGGATGAA	GCAGATAGTG	AGGAAAAGTTG	AGCCAATAAT	180
GACGTGAAGT	CCGTGGAAGC	CTGTGGCTAC	AAAAAATGTT	GAGCCGTAGA	TGCCGTCGGA	240
AATGGTGAAG	GGAGACTCGA	AGTACTCTGA	GGCTTG TAGG	AGGGTAAAAT	AGAGACCCAG	300
TAAAATTGTA	ATAAGCAGTG	CTTGAATTAT	TTGGTTTCGG	TTGTTTTCTA	TTAGACTATG	360
GTGAGCTCAG	GTGATTGATA	CTCCTGATGC	GAGTAATACG	GATGTGTTTA	GGAGTGGGAC	420
TTCTAGGGGA	TTTAGCGGGG	TGATGCCTGT	TGGGGGCCAG	TGCCCTCCTA	GTTGGGGGGT	480
AGGGGCTAGG	CTGGAGTGGT	AAAAGGCTCA	GAAAAATCCT	GCGAAGAAAA	AAACTTCTGA	540
GGTAATAAAT	AGGATTATCC	CGTATCGAAG	GCCTTTTTGG	ACAGGTGGTG	TGTGGTGGCC	600
TTGGTATGTG	CTTCTCGTG	TTACATCGCG	CCATCATTGG	TATATGGTTA	GTGTGTTGGG	660
TTANTANGGC	CTANTATGAA	GAACTTTTGG	ANTGGAATTA	AATCAATNGC	TTGGCCGGAA	720
GTCAATTANGA	NGGCTNAAAA	GGCCCTGTTA	NGGGTCTGGG	CTNGGTTTTA	CCCNACCCAT	780
GGAATNCNCC	CCCCGGACNA	NTGNATCCCT	ATTCTTAA			818

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TTTTTTTTTT	TTTTTTTTTT	TGGCTCTAGA	GGGGGTAGAG	GGGGTGCTAT	AGGGTAAATA	60
CGGGCCCTAT	TTCAAAGATT	TTTAGGGGAA	TTAATTCTAG	GACGATGGGT	ATGAAACTGT	120
GGTTTGCTCC	ACAGATTTCA	GAGCATTGAC	CGTAGTATAC	CCCCGGTCGT	GTAGCGGTGA	180
AAGTGGTTTG	GTTTAGACGT	CCGGGAATTG	CATCTGTTTT	TAAGCCTAAT	GTGGGGACAG	240
CTCATGAGTG	CAAGACGTCT	TGTGATGTAA	TTATTATACN	AATGGGGGCT	TCAATCGGGA	300

GTACTACTCG	ATTGTCAACG	TCAAGGAGTC	GCAGGTCGCC	TGGTTCTAGG	AATAATGGGG	360
GAAGTATGTA	GGAATTGAAG	ATTAATCCGC	CGTAGTCGGT	GTTCTCCTAG	GTTCAATACC	420
ATTGGTGGCC	AATTGATTTG	ATGGTAAGGG	GAGGGATCGT	TGAACTCGTC	TGTTATGTAA	480
AGGATNCCTT	NGGGATGGGA	AGGCNATNAA	GGACTANGGA	TNAATGGCGG	GCANGATATT	540
TCAAACNGTC	TCTANTTCCT	GAAACGTCTG	AAATGTTAAT	AANAATTAAN	TTTNGTTATT	600
GAATNTTNNG	GAAAAGGGCT	TACAGGACTA	GAAACCAAAT	ANGAAAANTA	ATNNTAANGG	660
CNTTATCNTN	AAAGGTNATA	ACCNCTCCTA	TNATCCCACC	CAATNGNATT	CCCCACNCNN	720
ACNATTGGAT	NCCCCANTTC	CANAAANGGC	CNCCCCCGG	TGNANNCCNC	CTTTTGTTC	780
CTTNANTGAN	GGTTATTNC	CCCTNGCNTT	ATCANCC			817

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CATTTCCGGG	TTTACTTTCT	AAGGAAAGCC	GAGCGGAAGC	TGCTAACGTG	GGAATCGGTG	60
CATAAGGAGA	ACTTTCTGCT	GGCACGCGCT	AGGACAAGC	GGGAGAGCGA	CTCCGAGCGT	120
CTGAAGCGCA	CGTCCCAGAA	GGTGGACTTG	GCACTGAAAC	AGCTGGGACA	CATCCGCGAG	180
TACGAACAGC	GCCTGAAAGT	GCTGGAGCGG	GAGGTCCAGC	AGTGTAGCCG	CGTCCTGGGG	240
TGGGTGGCCG	ANGCCTGANC	CGCTCTGCCT	TGCTGCCCCC	ANGTGGGCCG	CCACCCCTTG	300
ACCTGCCTGG	GTCCAAACAC	TGAGCCCTGC	TGGCGGACTT	CAAGGANAAC	CCCCACANGG	360
GGATTTTGCT	CCTANANTAA	GGCTCATCTG	GGCCTCGGCC	CCCCCACCTG	GTTGGCCTTG	420
TCTTTGANGT	GAGCCCCATG	TCCATCTGGG	CCACTGTCNG	GACCACCTTT	NGGGAGTGTT	480
CTCCTTACAA	CCACANNATG	CCCGGCTCCT	CCCGGAAACC	ANTCCCANCC	TGNGAAGGAT	540
CAAGNCCTGN	ATCCACTNNT	NCTANAACCG	GCCNCCNCCG	CNGTGGAACC	CNCCTTNTGT	600
TCCTTTTCNT	TNAGGGTTAA	TNNCGCCTTG	GCCTTNCCAN	NGTCCTNCNC	NTTTTCCNNT	660
GTTNAAATTG	TTANGCNCCC	NCCNNTCCCN	CNNCNMCNAN	CCCGACCCNN	ANNTTNNANN	720
NCCTGGGGGT	NCCNNCNGAT	TGACCCNCC	NCCCTNTANT	TGCNTTNGGG	NNCNNTGCC	780
CTTCCCTCT	NGGGANNCG					799

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 801 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ACGCCTTGAT	CCTCCCAGGC	TGGGACTGGT	TCTGGGAGGA	GCCGGGCATG	CTGTGGTTTG	60
TAANGATGAC	ACTCCCAAAG	GTGGTCCTGA	CAGTGGCCCA	GATGGACATG	GGGCTCACCT	120
CAAGGACAAG	GCCACCAGGT	GCGGGGGCCG	AAGCCACAT	GATCCTTACT	CTATGAGCAA	180
AATCCCCTGT	GGGGGCTTCT	CCTGAAGTC	CGCCANCAGG	GCTCAGTCTT	TGGACCCANG	240
CAGGTCATGG	GGTTGTNGNC	CAACTGGGGG	CCNCAACGCA	AAANGGCNCA	GGGCCTCNGN	300
CACCCATCCC	ANGACGCGGC	TACACTNCTG	GACCTCCNC	TCCACCACTT	TCATGCGCTG	360

TTCNTACCCG	CGNATNTGTC	CCANCTGTTT	CNGTGCCNAC	TCCANCTTCT	NGGACGTGCG	420
CTACATACGC	CCGGANTCNC	NCTCCGCTT	TGTCCCTATC	CACGTNCCAN	CAACAAATTT	480
CNCCNTANTG	CACCNATTCC	CACNTTTTNNC	AGNTTTCNC	NNCGNGCTTC	CTTNTAAAAG	540
GGTTGANCCC	CGGAAAATNC	CCCAAAGGGG	GGGGGCCNGG	TACCCAACTN	CCCCCTNATA	600
GCTGAANTCC	CCATNACCNN	GNCTCNATGG	ANCCNTCCNT	TTTAANNACN	TTCTNAACTT	660
GGGAANANCC	CTCGNCCNTN	CCCCCNTTAA	TCCCNCTTG	CNANGNNCNT	CCCCCNNTCC	720
NCCCNNTNG	GCNTNTNANN	CNAAAAGGC	CCNNNANCAA	TCTCCTNNCN	CCTCANTTCG	780
CCANCCCTCG	AAATCGGCCN	C				801

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 789 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CAGTCTATNT	GGCCAGTGTG	GCAGCTTTC	CTGTGGCTGC	CGGTGCCACA	TGCCTGTCCC	60
ACAGTGTGGC	CGTGGTGACA	GCTTCAGCCG	CCCTCACCGG	GTTACCTTC	TCAGCCCTGC	120
AGATCCTGCC	CTACACACTG	GCCTCCCTCT	ACCACCGGGA	GAAGCAGGTG	TTCCTGCCCCA	180
AATACCGAGG	GGACACTGGA	GGTGCTAGCA	GTGAGGACAG	CCTGATGACC	AGCTTCCTGC	240
CAGGCCCTAA	GCCTGGAGCT	CCCTTCCCTA	ATGGACACGT	GGGTGCTGGA	GGCAGTGGCC	300
TGCTCCCACC	TCCACCCGCG	CTCTGCGGGG	CCTCTGCCTG	TGATGTCTCC	GTACGTGTGG	360
TGGTGGGTGA	GCCCACCGAN	GCCAGGGTGG	TTCCGGGCGG	GGGCATCTGC	CTGGACCTCG	420
CCATCCTGGA	TAGTGCTTCC	TGCTGTCCCA	NGTGGCCCCA	TCCCTGTTTA	TGGGCTCCAT	480
TGTCCAGCTC	AGCCAGTCTG	TCACTGCCTA	TATGGTGTCT	GCCGCAGGCC	TGGGTCTGGT	540
CCCATTACT	TTGCTACACA	GGTANTATT	GACAAGAACG	ANTTGGCCAA	ATACTCAGCG	600
TTAAAAAATT	CCAGCAACAT	TGGGGGTGGA	AGGCCTGCCT	CACTGGGTCC	AACTCCCCGC	660
TCCTGTTAAC	CCCATGGGGC	TGCCGGCTTG	GCCGCCAATT	TCTGTTGCTG	CCAAANTNAT	720
GTGGCTCTCT	GCTGCCACCT	GTTGCTGGCT	GAAGTGCNTA	CNGCNCANCT	NGGGGGGTNG	780
GGNGTTCCC						789

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 772 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CCCACCTTAC	CCAAATATTA	GACACCAACA	CAGAAAAGCT	AGCAATGGAT	TCCCTTCTAC	60
TTTGTAAAT	AAATAAGTTA	AATATTTAAA	TGCCTGTGTC	TCTGTGATGG	CAACAGAAGG	120
ACCAACAGGC	CACATCCTGA	TAAAAGGTAA	GAGGGGGGTG	GATCAGCAAA	AAGACAGTGC	180
TGTGGGCTGA	GGGGACCTGG	TTCTTGTGTG	TTGCCCCCTCA	GGACTCTTCC	CCTACAAATA	240
ACTTTCATAT	GTTCAAATCC	CATGGAGGAG	TGTTTCATCC	TAGAACTCC	CATGCAAGAG	300
CTACATTAAA	CGAAGCTGCA	GGTTAAGGGG	CTTANAGATG	GGAAACCAGG	TGACTGAGTT	360
TATTCAGCTC	CCAAAAACCC	TTCTCTAGGT	GTGTCTCAAC	TAGGAGGCTA	GCTGTTAACC	420

CTGAGCCTGG	GTAATCCACC	TGCAGAGTCC	CCGCATTCCA	GTGCATGGAA	CCCTTCTGGC	480
CTCCCTGTAT	AAGTCCAGAC	TGAAACCCCC	TTGGAAGGNC	TCCAGTCAGG	CAGCCCTANA	540
AACTGGGGAA	AAAAGAAAAG	GACGCCCCAN	CCCCCAGCTG	TGCANCTACG	CACCTCAACA	600
GCACAGGGTG	GCAGCAAAAA	AACCACTTTA	CTTTGGCACA	AACAAAAACT	NGGGGGGGCA	660
ACCCCGGCAC	CCCNANGGGG	GTTAACAGGA	ANCNGGGNAA	CNTGGAACCC	AATTNAGGCA	720
GGCCCNCCAC	CCCNAAATNTT	GCTGGGAAAT	TTTTCTCCCC	CTAAATTNTT	TC	772

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GCCCCAATTC	CAGCTGCCAC	ACCACCCACG	GTGACTGCAT	TAGTTCGGAT	GTCATACAAA	60
AGCTGATTGA	AGCAACCCTC	TACTTTTTTG	TCGTGAGCCT	TTTGCTTGGT	GCAGGTTTCA	120
TTGGCTGTGT	TGGTGACGTT	GTCATTGCAA	CAGAATGGGG	GAAAGGCACT	GTTCTCTTTG	180
AAGTANGGTG	AGTCCTCAAA	ATCCGTATAG	TTGGTGAAGC	CACAGCACTT	GAGCCCTTTC	240
ATGGTGGTGT	TCCACACTTG	AGTGAAGTCT	TCCTGGGAAC	CATAATCTTT	CTTGATGGCA	300
GGCACTACCA	GCAACGTCAG	GGAAGTGCTC	AGCCATTGTG	GTGTACACCA	AGGCGACCAC	360
AGCAGCTGCN	ACCTCAGCAA	TGAAGATGAN	GAGGANGATG	AAGAAGAACG	TCNCGAGGGC	420
ACACTTGCTC	TCAGTCTTAN	CACCATANCA	GCCCNTGAAA	ACCAANANCA	AAGACCACNA	480
CNCCGGCTGC	GATGAAGAAA	TNACCCNCG	TTGACAAACT	TGCATGGCAC	TGGGANCCAC	540
AGTGGCCCN	AAAATCTTCA	AAAAGGATGC	CCCATCNATT	GACCCCCCAA	ATGCCCACTG	600
CCAACAGGGG	CTGCCCCACN	CNCNNAACGA	TGANCCNATT	GNACAAGATC	TNCNTGGTCT	660
TNATNAACNT	GAACCTGTCN	TNGTGGCTCC	TGTTTCAGGNC	CNNGGCCTGA	CTTCTNAANN	720
AANGAACTCN	GAAGNCCCCA	CNGGANANNC	G			751

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 729 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GAGCCAGGCG	TCCCTCTGCC	TGCCCCACTCA	GTGGCAACAC	CCGGGAGCTG	TTTTGTCTTT	60
TGTGGANCCCT	CAGCAGTNCC	CTCTTTTCTG	ACTCANTGCC	AAGANCCCTG	AACAGGAGCC	120
ACCATGCAGT	GCTTCAGCTT	CATTAAAGACC	ATGATGATCC	TCTTCAATTT	GCTCATCTTT	180
CTGTGTGGTG	CAGCCCTGTT	GGCAGTGGGC	ATCTGGGTGT	CAATCGATGG	GGCATCCTTT	240
CTGAAGATCT	TCGGGGCACT	GTCGTCCAGT	GCCATGCAGT	TTGTCAACGT	GGGCTACTTC	300
CTCATCGCAG	CCGGCGTTGT	GGTCTTAGCT	CTAGGTTTCC	TGGGCTGCTA	TGGTGCTAAG	360
ACTGAGAGCA	AGTGTGCCCT	CGTGACGTTT	TTCTTCATCC	TCCTCCTCAT	CTTCATTGCT	420
GAGGTTGCAA	TGCTGTGGTC	GCCTTGGTGT	ACACCACAAT	GGCTGAGCAC	TTCCTGACGT	480
TGCTGGTAAT	GCCTGCCATC	AANAAAAGAT	TATGGGTTCC	CAGGAANACT	TCACTCAAGT	540
GTTGGAACAC	CACCATGAAA	GGGCTCAAGT	GCTGTGGCTT	CNNCCAATA	TACGGATTTT	600

GAAGANTCAC	CTACTTCAAA	GAAAAAGTG	CCTTTCCCCC	ATTTCTGTTG	CAATTGACAA	660
ACGTCCCCAA	CACAGCCAAT	TGAAAACCTG	CACCCAACCC	AAANGGGTCC	CCAACCANAA	720
ATTNAAGGG						729

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TGCTCTTCCT	CAAAGTTGTT	CTTGTTGCCA	TAACAACCAC	CATAGGTAAA	GCGGGCGCAG	60
TGTTTCGCTGA	AGGGGTGTA	GTACCAGCGC	GGGATGCTCT	CCTTGCAGAG	TCCTGTGTCT	120
GGCAGGTCCA	CGCAGTGCCC	TTTGTCACTG	GGGAAATGGA	TGCGCTGGAG	CTCGTCAAAG	180
CCACTCGTGT	ATTTTTCACA	GGCAGCCTCG	TCCGACGCGT	CGGGGCAGTT	GGGGGTGTCT	240
TCACACTCCA	GGAAACTGTC	NATGCAGCAG	CCATTGCTGC	AGCGGAACTG	GGTGGGCTGA	300
CANGTGCCAG	AGCACACTGG	ATGGCGCCTT	TCCATGNNAN	GGGCCCTGNG	GGAAAGTCCC	360
TGANCCCCAN	ANCTGCCTCT	CAAANGCCCC	ACCTTGACACA	CCCCGACAGG	CTAGAATGGA	420
ATCTTCTTCC	CGAAAGGTAG	TTNTTCTTGT	TGCCCAANCC	ANCCCCNTAA	ACAAACTCTT	480
GCANATCTGC	TCCGNGGGGG	TCNTANTACC	ANCGTGGGAA	AAGAACCCCA	GGCNGCGAAC	540
CAANCTTGTT	TGGATNCGAA	GCNATAATCT	NCTNTTCTGC	TTGGTGGACA	GCACCANTNA	600
CTGTNNANCT	TTAGNCCNTG	GTCCTCNTGG	GTTGNNTTGG	AACCTAATCN	CCNNTCAACT	660
GGGACAAGGT	AANTNGCCNT	CCTTTNAATT	CCCNANCNTN	CCCCCTGGTT	TGGGGTTTTN	720
CNCNCTCCTA	CCCCAGAAAN	NCCGTGTTCC	CCCCCAACTA	GGGGCCNAAA	CCNNTTNTTC	780
CACAACCCTN	CCCCACCCAC	GGTTCNGNT	GTTNG			816

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 783 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCAAGGCCTG	GGCAGGCATA	NACTTGAAGG	TACAACCCCA	GGAACCCCTG	GTGCTGAAGG	60
ATGTGGAAAA	CACAGATTGG	CGCCTACTGC	GGGGTGACAC	GGATGTCAGG	GTAGAGAGGA	120
AAGACCCAAA	CCAGGTGGAA	CTGTGGGGAC	TCAAGGAANG	CACCTACCTG	TTCCAGCTGA	180
CAGTGACTAG	CTCAGACCAC	CCAGAGGACA	CGGCCAACGT	CACAGTCACT	GTGCTGTCCA	240
CCAAGCAGAC	AGAAGACTAC	TGCCTCGCAT	CCAACAANGT	GGGTCGCTGC	CGGGGCTCTT	300
TCCCACGCTG	GTACTATGAC	CCCACGGAGC	AGATCTGCAA	GAGTTTCGTT	TATGGAGGCT	360
GCTTGGGCAA	CAAGAACAAC	TACCTTCGGG	AAGAAGAGTG	CATTCTANCC	TGTCNNGGTG	420
TGCAAGGTGG	GCCTTTGANA	NGCANCTCTG	GGGCTCANGC	GACTTTCCCC	CAGGGCCCCCT	480
CCATGGAAAG	GCGCCATCCA	NTGTTCTCTG	GCACCTGTCA	GCCCACCCAG	TTCCGCTGCA	540
NCAATGGCTG	CTGCATCNAC	ANTTTCCTNG	AATTGTGACA	ACACCCCCCA	NTGCCCCCAA	600
CCCTCCCAAC	AAAGCTTCCC	TGTTNAAAAA	TACNCCANTT	GGCTTTTNAC	AAACNCCCGG	660
CNCCTCCNTT	TTCCCNNTN	AACAAAGGGC	NCTNGCNTTT	GAAGTGGCCN	AACCCNGGAA	720

TCTNCCNNGG AAAAANTNCC CCCCCTGGTT CCTNNAANCC CCTCCNCNAA ANCTNCCCCC 780
 CCC 783

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 801 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GCCCCAATTC	CAGCTGCCAC	ACCACCCACG	GTGACTGCAT	TAGTTCGGAT	GTCATACAAA	60
AGCTGATTGA	AGCAACCCTC	TACTTTTTGG	TCGTGAGCCT	TTTGCTTGGT	GCAGGTTTCA	120
TTGGCTGTGT	TGGTGACGTT	GTCATTGCAA	CAGAATGGGG	GAAAGGCACT	GTTCTCTTTG	180
AAGTAGGGTG	AGTCCTCAAA	ATCCGTATAG	TTGGTGAAGC	CACAGCACTT	GAGCCCTTTC	240
ATGGTGGTGT	TCCACACTTG	AGTGAAGTCT	TCCTGGGAAC	CATAATCTTT	CTTGATGGCA	300
GGCACTACCA	GCAACGTCAG	GAAGTGCTCA	GCCATTGTGG	TGTACACCAA	GGCGACCACA	360
GCAGTGCAA	CCTCAGCAAT	GAAGATGAGG	AGGAGGATGA	AGAAGAACGT	CNCGAGGGCA	420
CACTTGCTCT	CCGTCTTAGC	ACCATAGCAG	CCCANGAAAC	CAAGAGCAAA	GACCACAACG	480
CCNGCTGCGA	ATGAAAGAAA	NTACCCACGT	TGACAAACTG	CATGGCCACT	GGACGACAGT	540
TGGCCCGAAN	ATCTTCAGAA	AAGGGATGCC	CCATCGATTG	AACACCCANA	TGCCCCACTGC	600
CNACAGGGCT	GCNCCNCNCN	GAAAGAATGA	GCCATTGAAG	AAGGATCNTC	NTGGTCTTAA	660
TGAACTGAAA	CCNTGCATGG	TGGCCCTGT	TCAGGCTCT	TGGCAGTGAA	TTCTGANAAA	720
AAGGAACNGC	NTNAGCCCCC	CCAAANGANA	AAACACCCCC	GGGTGTTGCC	CTGAATTGGC	780
GGCCAAGGAN	CCCTGCCCCN	G				801

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 740 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GTGAGAGCCA	GGCGTCCCTC	TGCCTGCCCA	CTCAGTGCCA	ACACCCGGGA	GCTGTTTTGT	60
CCTTTGTGGA	GCCTCAGCAG	TTCCTCTTTT	CAGAACTCAC	TGCCAAGAGC	CCTGAACAGG	120
AGCCACCATG	CAGTGCTTCA	GCTTCATTAA	GACCATGATG	ATCCTCTTCA	ATTTGCTCAT	180
CTTTCTGTGT	GGTGCAGCCC	TGTTGGCAGT	GGGCATCTGG	GTGTCAATCG	ATGGGGCATC	240
CTTTCTGAAG	ATCTTCGGGC	CACTGTCGTC	CAGTGCCATG	CAGTTTGTC	ACGTGGGCTA	300
CTTCCTCATC	GCAGCCGGCG	TTGTGGTCTT	TGCTCTTGGT	TTCTTGGGCT	GCTATGGTGC	360
TAAGACGGAG	AGCAAGTGTG	CCCTCGTGAC	GTTCTTCTTC	ATCCTCCTCC	TCATCTTCAT	420
TGCTGAAGTT	GCAGCTGCTG	TGCTGCCTT	GGTGTAACC	ACAATGGCTG	AACCATTCCT	480
GACGTTGCTG	GTANTGCCTG	CCATCAANAA	AGATTATGGG	TTCCCAGGAA	AAATTCACTC	540
AANTNTGGAA	CACCNCCATG	AAAAGGGCTC	CAATTCTGN	TGGCTTCCCC	AACTATACCG	600
GAATTTTGAA	AGANTCNCCC	TACTTCCAAA	AAAAAANANT	TGCCTTTNCC	CCCNTTCTGT	660
TGCAATGAAA	ACNTCCCAAN	ACNGCCAATN	AAAACCTGCC	CNNNCAAAAA	GGNTCNCAAA	720
CAAAAAAANT	NNAAGGGTTN					740

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 802 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

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CCGCTGGTTG CGCTGGTCCA GNGNAGCCAC GAAGCACGTC AGCATAACACA GCCTCAATCA      60
CAAGGTCTTC CAGCTGCCGC ACATTACGCA GGGCAAGAGC CTCCAGCAAC ACTGCATATG    120
GGATACACTT TACTTTAGCA GCCAGGTGA CAACTGAGAG GTGTCGAAGC TTATTCTTCT    180
GAGCCTCTGT TAGTGGAGGA AGATTCCGGG CTTCAGCTAA GTAGTCAGCG TATGTCCCAT    240
AAGCAAACAC TGTGAGCAGC CGGAAGGTAG AGGCAAAGTC ACTCTCAGCC AGCTCTCTAA    300
CATTGGGCAT GTCCAGCAGT TCTCCAAACA CGTAGACACC AGNGGCCTCC AGCACCTGAT    360
GGATGAGTGT GGCCAGCGCT GCCCCCTTGG CCGACTTGGC TAGGAGCAGA AATTGCTCCT    420
GGTTCTGCCC TGTCACCTTC ACTTCCGCAC TCATCACTGC ACTGAGTGTG GGGGACTTGG    480
GCTCAGGATG TCCAGAGACG TGGTTCGCC CCCTCNCTTA ATGACACCGN CCANCAACC      540
GTCGGTCCC GCCGANTGNG TTCGTCGTNC CTGGGTCAGG GTCTGCTGGC CNCTACTTGC    600
AANCTTCGTC NGGCCCATGG AATTCACCNC ACCGGAAC TNANGATCCA CTNNTTCTAT    660
AACC GGNCGC CACCGC NNTT GGAATCCAC TCTTNTTNC TTTACTTGAG GGTAAAGTGC    720
ACCCTTNNCG TTACCTTGGT CCAAACNTN CCNTGTGTCG ANATNGTNAA TCNGGNCCNA    780
TNCCANCCNC ATANGAAGCC NG

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(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 731 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

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CNAAGCTTCC AGGTNACGGG CCGCNAANCC TGACCCNAGG TANCANAANG CAGNCNGCGG      60
GAGCCCACCG TCACGNGGNG GNGTCTTTAT NGGAGGGGGC GGAGCCACAT CNCTGGACNT    120
CNTGACCCCA ACTCCCNCC NCNCANTGCA GTGATGAGTG CAGAACTGAA GGTNACGTGG    180
CAGGAACCAA GANCAAANNC TGCTCCNNTC CAAGTCGGCN NAGGGGGCGG GGCTGGCCAC    240
GCNCATCCNT CNAGTGCTGN AAAGCCCCNN CCTGTCTACT TGTTTGGAGA ACNGC NNGA    300
CATGCCCAGN GTTANATAAC NGGCNGAGAG TNANTTTGCC TCTCCCTTCC GGCTGCGCAN    360
CGNGTNTGCT TAGNGGACAT AACCTGACTA CTTAAC TGAA CCCNNGAATC TNCCNCCCCT    420
CCACTAAGCT CAGAACAAAA AACTTCGACA CCACTCANTT GTCACCTGNC TGCTCAAGTA    480
AAGTGTACCC CATNCCCAAT GTNTGCTNGA NGCTCTGNCC TGCNTTANGT TCGGTCTTGG    540
GAAGACCTAT CAATTNAAAG TATGTTTCTG ACTGCCTCTT GCTCCCTGNA ACAANCNACC    600
CNNCNNTCCA AGGGGGGGNC GGCCCCCAAT CCCCCCAACC NTNAATTNAN TTTANCCCCN    660
CCCCNGGCC CGGCCTTTTA CNANCNTCNN NNACNGGGNA AAACCNNGC TTTNCCCAAC    720
NNAATCCNCC T

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(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 754 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

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TTTTTTTTTT TTTTTTTTTT TAAAAACCCC CTCCATTNAA TGNAAACTTC CGAAATTGTC      60
CAACCCCTC NTCCAAATNN CCNTTCCGG GNGGGGGTTC CAAACCAAN TTANNTTTGG      120
ANNTTAAATT AAATNTNNT TGGNGGNNA ANCCNAATGT NANGAAAGTT NAACCCANTA      180
TNANCTNAA TNCCTGAAA CCNGTNGNTT CCAAAAAATNT TTAACCTTA ANTCCCTCCG      240
AAATNGTTNA NGGAAAACCC AANTTCTCNT AAGGTTGTTT GAAGGNTNAA TNAAAANCCC      300
NNCCAATTGT TTTTNGCCAC GCCTGAATTA ATTGGNTTCC GNTGTTTTC NTTAAAANAA      360
GGNNANCCCC GGTANTNAA TCCCCCNCC CCAATTATA CCGANTTTT TTNGAATTGG      420
GANCCNCGG GAATTAACGG GGNNNTCCC TTTGGGGGG CNGGNNCCCC CCCCNTCGGG      480
GGTTNGGGNC AGGNCNNAAT TGTTTAAGGG TCCGAAAAAT CCCTCCNAGA AAAAAANCTC      540
CCAGGTGAG NNTNGGTTT NCCCCCCCC CANGGCCCT CTCGNANAGT TGGGGTTTGG      600
GGGGCCTGGG ATTTTNTTTC CCTTNTNCC TCCCCCCCC CCNGGGANAG AGGTTNGNGT      660
TTTGNTCNNC GGCCCNCCN AAGANCTTN CCGANTTNAN TTAAATCCNT GCCTNGGCGA      720
AGTCNTTGN AGGGNTAAAN GGCCCCCTNN CGGG                                754

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(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 755 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

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ATCANCCCAT GACCCNAAC NNGGGACCNC TCANCCGGNC NNNCNACCNC CGGCCNATCA      60
NNGTNAGNNC ACTNCNNTN NATCACNCCC CNCCNACTAC GCCCNANANC CNACGCNCTA      120
NNCANATNCC ACTGANNGCG CGANGTNGAN NGAGAAANCT NATACCANAG NCACCANACN      180
CCAGCTGTCC NANAANGCCT NNNATACNGG NNNATCCAAT NTGNANCCTC CNAAGTATTN      240
NNCNANANAT GATTTTCCTN ANCCGATTAC CCNTNCCCC TANCCCCCTC CCCCCAACNA      300
CGAAGGCNCT GGNCNAAGG NNGCGNCNCC CCGCTAGNTC CCCNCAAGT CNCNCNCCTA      360
AACTCANCCN NATTACNCGC TTCNTGAGTA TACTCCCCG AATCTCACC TACTCAACTC      420
AAAAANATCN GATACAAAAT AATNCAAGCC TGNTTATNAC ACTNTGACTG GGTCTCTATT      480
TTAGNGGTCC NTNAANCNTC CTAATACTTC CAGTCTNCCT TCNCCAATT CCNAANGGCT      540
CTTTCNGACA GCATNTTTTG GTTCCNNTT GGGTCTTAN NGAATTGCC TTCNTNGAAC      600
GGGCTCNTCT TTTCTTCGG TTANCCTGGN TTCNCCGGC CAGTTATTAT TTCCNTTTT      660
AAATTCNTNC CNTTANTTT TGGCNTTCNA ACCCCCGGC CTTGAAAACG GCCCCCTGGT      720
AAAAGGTTGT TTTGANAAAA TTTTGTTTT GTTCC                                755

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(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 849 base pairs

- (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TTTTTTTTTT	TTTTTANGTG	TNGTCGTGCA	GGTAGAGGCT	TACTACAANT	GTGAANACGT	60
ACGCTNGGAN	TAANGCGACC	CGANTTCTAG	GANNNCNCCCT	AAAATCANAC	TGTGAAGATN	120
ATCCTGNNNA	CGGAANGGTC	ACCGGNNGAT	NNTGCTAGGG	TGNCCNCTCC	CANNNCNTTN	180
CATAACTCNG	NGGCCCTGCC	CACCACCTTC	GGCGGCCCCNG	NGNCCGGGCC	CGGGTCATTN	240
GNNTTAACCN	CACTNNGCNA	NCGGTTTCCN	NCCCCNNCNG	ACCCNNGGCGA	TCCGGGGTNC	300
TCTGTCTTCC	CCTGNAGNCN	ANAAANTGGG	CCNCGGNCCC	CTTTACCCCT	NNACAAGCCA	360
CNGCCNTCTA	NCCNCNGCCC	CCCCTCCANT	NNGGGGGACT	GCCNANNGCT	CCGTTNCTNG	420
NNACCCCNNN	GGGTNCCTCG	GTTGTGANT	CNACCGNANG	CCANGGATTC	CNAAGGAAGG	480
TGCGTTNTTG	GCCCCTACCC	TTCGCTNCGG	NNCACCTTTC	CCGACNANGA	NCCGCTCCCG	540
CNCNCGNNG	CCTCNCCTCG	CAACACCCGC	NCTCNCNGT	NCGGNNNCCC	CCCCACCCGC	600
NCCCTCNCNC	NGNCGNANCN	CTCCNCCNCC	GTCTCANNCA	CCACCCCGCC	CCGCCAGGCC	660
NTCANCCACN	GGNNGACNNG	NAGCNCNNTC	GCNCCGCGCN	GCGNCNCCCT	CGCCNCNGAA	720
CTNCNTCNGG	CCANTNNGCG	TCAANCCNNA	CNAAACGCCG	CTGCGCGGCC	CGNAGCGNCC	780
NCCTCCNCGA	GTCTCCCGN	CTTCCNACCC	ANGNNTTCCN	CGAGGACACN	NNACCCCGCC	840
NNCANGCGG						849

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 872 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GCGCAAATA	TACTTCGCTC	GNACTCGTGC	GCCTCGCTNC	TCTTTTCCTC	CGCAACCATG	60
TCTGACNANC	CCGATTNGGC	NGATATCNAN	AAGNTCGANC	AGTCCAAACT	GANTAACACA	120
CACACNCNAN	AGANAAATCC	NCTGCCTTCC	ANAGTANACN	ATTGAACNNG	AGAACCANGC	180
NGGCGAATCG	TAATNAGGCG	TGCGCCGCCA	ATNTGTCNCC	GTTTATTNTN	CCAGCNTCNC	240
CTNCCNACCC	TACNTCTTCN	NAGCTGTCNN	ACCCCTNGTN	CGNACCCCCC	NAGGTCGGGA	300
TCGGGTTTNN	NNTGACCGNG	CNNCCCTCC	CCCCNTCCAT	NACGANCCNC	CCGCACCACC	360
NANNGCNCGC	NCCCCGNNCT	CTTCGCCNCC	CTGTCTTNTN	CCCCTGTNGC	CTGGCNCNGN	420
ACCGCATTGA	CCCTCGCCNN	CTNCNNGAAA	NCGNANACGT	CCGGGTGNN	ANNANCGCTG	480
TGGGNMNGCG	TCTGCNCCGC	GTTCCTTCCN	NCNNCTTCCA	CCATCTTCNT	TACNGGGTCT	540
CCNCGCCNTC	TCNNNCACNC	CCTGGGACGC	TNTCCTNTGC	CCCCCTTNAC	TCCCCCCTT	600
CGNCGTGNC	CGNCCCCACC	NTCATTNCA	NACGNTCTTC	ACAANNNCCT	GGNTNNCTCC	660
CNANCNGNCN	GTCAANCCNAG	GGAAGGGNGG	GGNCCNNTG	NTTGACGTTG	NGGNGANGTC	720
CGAANANTCC	TCNCCNTCAN	CNCTACCCCT	CGGCGGNCT	CTCNGTTNCC	AACTTANCAA	780
NTCTCCCCCG	NGNGCNCNTC	TCAGCCTCNC	CNCCCCNCT	CTCTGCANTG	TNCTCTGCTC	840
TNACCNTAC	GANTNTTCGN	CNCCCTCTTT	CC			872

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 815 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

```
GCATGCAAGC TTGAGTATTC TATAGNGTCA CCTAAATANC TTGGCNTAAT CATGGTCNTA      60
NCTGNCTTCC TGTGTCAAAT GTATACNAAN TANATATGAA TCTNATNTGA CAAGANNGTA      120
TCNTNCATTA GTAACAANTG TNNTGTCCAT CCTGTGNGAN CANATTCCCA TMNATTNCGN      180
CGCATTNCN GCNCANTATN TAATNGGGAA NTCNNNTNNN NCACCNNCAT CTATCNTNCC      240
GCNCCCTGAC TGGNAGAGAT GGATNANTTC TNNTNTGACC NACATGTTCA TCTTGGATTN      300
AANANCCCC CGCNGNCCAC CGGTTNGNNG CNAGCCNNTC CCAAGACCTC CTGTGGAGGT      360
AACCTGCGTC AGANNCATCA AACNTGGGAA ACCCGCNCNC ANGTNNAAGT NGNNNCANAN      420
GATCCCGTCC AGGNTTNACC ATCCCTTCNC AGCGCCCCCT TTNGTGCCTT ANAGNGNAGC      480
GTGTCCNANC CNCTCAACAT GANACGCGCC AGNCCANCCG CAATTNGGCA CAATGTCGNC      540
GAACCCCTA GGGGGANTNA TNCAAANCCC CAGGATTGTC CNCNCANGAA ATCCNCANC      600
CCNCCCTAC CCNCTTTGG GACNGTGACC AANTCCCGGA GTNCCAGTCC GGCCNGNCTC      660
CCCCACCGGT NNCCNTGGGG GGGTGAANCT CNGNNTCANC CNGNCGAGGN NTCGNAAGGA      720
ACCGGNCCTN GGNCGAANNG ANCNNTCNGA AGNGCCNCNT CGTATAACCC CCCCTCNCCA      780
NCCNACNGNT AGNTCCCCC CNGGGTNCGG AANGG                                815
```

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 775 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

```
CCGAGATGTC TCGCTCCGTG GCCTTAGCTG TGCTCGCGCT ACTCTCTCTT TCTGGCCTGG      60
AGGCTATCCA GCGTACTCCA AAGATTCAGG TTTACTCAGC TCATCCAGCA GAGAATGGAA      120
AGTCAAATTT CCTGAATTGC TATGTGTCTG GGTTCATCC ATCCGACATT GAANTTGAAT      180
TACTGAAGAA TGGANAGAGA ATTGAAAAAG TGGAGCATTG AGACTTGTCT TTCAGCAAGG      240
ACTGGTCTTT CTATCTCNTG TACTACACTG AATTCACCCC CACTGAAAAA GATGAGTATG      300
CCTGCCGTGT GAACCATGTG ACTTTGTCAC AGCCCAAGAT AGTTAAGTGG GATCGAGACA      360
TGTAAGCAGN CNNCATGGAA GTTTGAAGAT GCCGCATTG GATTGGATGA ATTCCAAATT      420
CTGCTTGCTT GCNTTTTAAT ANTGATATGC NTATACACCC TACCCTTTAT GNCCCCAAAT      480
TGTAGGGGTT ACATNANTGT TCNCTNNGGA CATGATCTTC CTTTATAANT CCNCCNTTCG      540
AATTGCCCCG CNCCCNNGTN NGAATGTTTC CNNAACCACG GTTGGCTCCC CCAGGTCNCC      600
TCTTACGGAA GGGCCTGGGC CNCTTTNCAA GGTGGGGGA ACCNAAAATT TCNCTTNTGC      660
CCNCCNCCA CNNTCTTGNG NNCNCANTTT GGAACCCCTC CNATTCCCTT TGGCCTCNNA      720
NCCTTNCTA ANAAAATTN AAANCGTNGC NAAANNTTN ACTTCCCCC TTACC              775
```

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 820 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

ANATTANTAC	AGTGTAATCT	TTTCCCAGAG	GTGTGTANAG	GGAACGGGGC	CTAGAGGCAT	60
CCCANAGATA	NCTTATANCA	ACAGTGCTTT	GACCAAGAGC	TGCTGGGCAC	ATTTCTTGCA	120
GAAAAGGTGG	CGGTCCCCAT	CACTCCTCCT	CTCCCATAGC	CATCCCAGAG	GGGTGAGTAG	180
CCATCANGCC	TTCGGTGGGA	GGGAGTCANG	GAAACAACAN	ACCACAGAGC	ANACAGACCA	240
NTGATGACCA	TGGGCGGGAG	CGAGCCTCTT	CCCTGNACCG	GGGTGGCANA	NGANAGCCTA	300
NCTGAGGGGT	CACACTATAA	ACGTTAACGA	CCNAGATNAN	CACCTGCTTC	AAGTGCACCC	360
TTCTTACCTG	ACNACCAGNG	ACCNNAACT	GCNGCCTGGG	GACAGCNCCTG	GGANCAGCTA	420
ACNNAGCACT	CACCTGCCCC	CCCATGGCCG	TNCGCNTCCC	TGGTCCTGNC	AAGGGAAGCT	480
CCCTGTTGGA	ATTNCGGGGA	NACCAAGGGA	NCCCCCTCCT	CCANCTGTGA	AGGAAAAANN	540
GATGGAATTT	TNCCCTTCCG	GCCNNTCCCC	TCTTCTTTTA	CACGCCCCCT	NNTACTCNTC	600
TCCCTCTNTT	NTCCTGNCNC	ACTTTTNACC	CCNNNATTTT	CCTTNATTGA	TCGGANNCTN	660
GANATTCCAC	TNNGCCTNC	CNTCNATCNG	NAANACNAAA	NACTNTCTNA	CCCGGGGAT	720
GGGNCCCTCG	NTCATCCTCT	CTTTTTCNCT	ACCNCCNNTT	CTTTGCCTCT	CCTTNGATCA	780
TCCAACNTC	GNTGGCCNTN	CCCCCCNNN	TCCTTTNCCC			820

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 818 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TCTGGGTGAT	GGCCTCTTCC	TCCTCAGGGA	CCTCTGACTG	CTCTGGGCCA	AAGAATCTCT	60
TGTTTCTTCT	CCGAGCCCCA	GGCAGCGGTG	ATTGAGCCCT	GCCCAACCTG	ATTCTGATGA	120
CTGCGGATGC	TGTGACGGAC	CCAAGGGGCA	AATAGGGTCC	CAGGGTCCAG	GGAGGGGCGC	180
CTGCTGAGCA	CTTCCGCCCC	TCACCCTGCC	CAGCCCCGTC	CATGAGCTCT	GGGCTGGGTC	240
TCCGCTCCA	GGGTTCTGCT	CTTCCANGCA	NGCCANCAAG	TGGCGCTGGG	CCACACTGGC	300
TTCTTCCTGC	CCCNTCCCTG	GCTCTGANTC	TCTGTCTTCC	TGTCCTGTGC	ANGCNCCTTG	360
GATCTCAGTT	TCCCTCNCTC	ANNGAACTCT	GTTTCTGANN	TCTTCANTTA	ACTNTGANTT	420
TATNACCNAN	TGGNCTGTNC	TGTCNNACTT	TAATGGGCCN	GACCGGCTAA	TCCCTCCCTC	480
NCTCCCTTCC	ANTTCNNNNA	ACCNGCTTNC	CNTCNTCTCC	CCNTANCCCG	CCNGGGAANC	540
CTCCTTTGCC	CTNACCANGG	GCCNNNACCG	CCCNTNNCTN	GGGGGGCNGG	GTNNCTNCNC	600
CTGNTNNCCC	CNCTCNCNNT	TNCCTCGTCC	CNNCNCNCGN	NNGCANNTTC	NCNGTCCCNN	660
TNNCTCTTCN	NGTNTCGNAA	NGNTCNCNTN	TNNNNNGNCN	NGNTNNTNCN	TCCCTCTCNC	720
CNNNTGNANG	TNNTTNNNNC	NCNGNNCCCC	NNNNCNNNNN	NGGNNNTNNN	TCTNCNCNGC	780
CCCNCCCCC	NGNATTAAGG	CCTCCNNTCT	CCGGCCNC			818

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 731 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AGGAAGGGCG	GAGGGATATT	GTANGGGATT	GAGGGATAGG	AGNATAANGG	GGGAGGTGTG	60
TCCCAACATG	ANGGTGNNGT	TCTCTTTTGA	ANGAGGGTTG	NGTTTTTANN	CCNGGTGGGT	120
GATTNAACCC	CATTGTATGG	AGNNAAAGGN	TTNAGGGAT	TTTTCGGCTC	TTATCAGTAT	180
NTANATTCCCT	GTNAATCGGA	AAATNATNTT	TCNNCNGGAA	AATNTTGCTC	CCATCCGNAA	240
ATTNCTCCCG	GGTAGTGCAT	NTTNGGGGGN	CNGCCANGTT	TCCCAGGCTG	CTANAATCGT	300
ACTAAAGNTT	NAAGTGGGAN	TNCAAATGAA	AACCTNNCAC	AGAGNATCCN	TACCCGACTG	360
TNNNTTNCCT	TCGCCCTNTG	ACTCTGCNNG	AGCCCAATAC	CCNNGNGNAT	GTCNCCCNGN	420
NNNGCGNCNC	TGAAANNNNC	TCGNGGCTNN	GANCATCANG	GGGTTTCGCA	TCAAAAGCNN	480
CGTTTCNCAT	NAAGGCACTT	TNGCCTCATC	CAACCNCTNG	CCCTCNNCCA	TTTNGCCGTC	540
NGGTTNCCT	ACGCTNNTNG	CNCCTNNNTN	GANATTTTNC	CCGCCTNGGG	NAANCCTCCT	600
GNAATGGGTA	GGGNCTTNTC	TTTTNACCNN	GNGGTNTACT	AATCNNCTNC	ACGCNTNCTT	660
TCTCNACCCC	CCCCCTTTT	CAATCCANC	GGCNAATGGG	GTCTCCCCNN	CGANGGGGGG	720
NNNCCANNC	C					731

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 822 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

ACTAGTCCAG	TGTGGTGGAA	TTCCATTGTG	TTGGGGNCNC	TTCTATGANT	ANTNTTAGAT	60
CGCTCANACC	TCACANCCTC	CCNACNANGC	CTATAANGAA	NANNAATAGA	NCTGTNCNNT	120
ATNTNTACNC	TCATANNCCT	CNNNACCCAC	TCCCTCTTAA	CCCNTACTGT	GCCTATNGCN	180
TNNCTANTCT	NTGCCGCCTN	CNANCCACCN	GTGGGCCNAC	CNCNNGNATT	CTCNATCTCC	240
TCNCCATNTN	GCCTANANTA	NGTNCATACC	CTATACCTAC	NCCAATGCTA	NNNCTAANCN	300
TCCATNANTT	ANNNTAACTA	CCACTGACNT	NGACTTTTNC	ATNANCTCCT	AATTGAATC	360
TACTCTGACT	CCACNGCCT	ANNNATTAGC	ANCNTCCCCC	NACNATNTCT	CAACCAAATC	420
NTCAACAACC	TATCTANCTG	TTCNCCAACC	NTTNCCTCCG	ATCCCCNNAC	AACCCCCCTC	480
CCAAATACCC	NCCACCTGAC	NCCTAACCCN	CACCATCCCG	GCAAGCCNAN	GGNCATTTAN	540
CCACTGGAAT	CACNATNGGA	NAAAAAAAAC	CCNAACTCTC	TANCNCNNAT	CTCCCTAANA	600
AATNCTCCTN	NAATTTACTN	NCANTNCCAT	CAANCCACN	TGAAACNNAA	CCCCTGTTTT	660
TANATCCCTT	CTTTCGAAAA	CCNACCCTTT	ANNNCCCAAC	CTTNGGGGCC	CCCCNCTNC	720
CCNAATGAAG	GNCNCCCAAT	CNANGAAACG	NCCNTGAAAA	ANCNAGGCNA	ANANNNTCCG	780
CANATCCTAT	CCCTTANTTN	GGGGNCCCTT	NCCCNGGGCC	CC		822

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 787 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CGGCCGCTG	CTCTGGCACA	TGCCTCCTGA	ATGGCATCAA	AAGTGATGGA	CTGCCCATTG	60
CTAGAGAAGA	CCTTCTCTCC	TACTGTCAAT	ATGGAGCCCT	GCAGACTGAG	GGCTCCCCTT	120
GTCTGCAGGA	TTTGATGTCT	GAAGTCGTGG	AGTGTGGCTT	GGAGCTCCTC	ATCTACATNA	180
GCTGGAAGCC	CTGGAGGGCC	TCTCTCGCCA	GCCTCCCCCT	TCTCTCCACG	CTCTCCANGG	240
ACACCAGGGG	CTCCAGGCAG	CCCATTATTC	CCAGNANGAC	ATGGTGTTC	TCCACGCGGA	300
CCCATGGGGC	CTGNAAGGCC	AGGGTCTCCT	TTGACACCAT	CTCTCCCGTC	CTGCCTGGCA	360
GGCCGTGGGA	TCCACTANTT	CTANAACGGN	CGCCACCNCG	GTGGGAGCTC	CAGCTTTTGT	420
TCCCNTTAAT	GAAGGTTAAT	TGCNCGCTTG	GCGTAATCAT	NGGTCANAAC	TNTTTCCTGT	480
GTGAAATTGT	TTNTCCCTC	NCNATTCNC	NCNACATACN	AACCCGGAAN	CATAAAGTGT	540
TAAAGCCTGG	GGGTNGCCTN	NNGAATNAAC	TNAACTCAAT	TAATTGCGTT	GGCTCATGGC	600
CCGCTTTCCN	TTCTNGGAAA	CTGTCTCCC	CTGCNTTNN	GAATCGGCCA	CCCCCNGGG	660
AAAAGCGGTT	TGCNTTTTNG	GGGGNTCCTT	CCNCTTCCCC	CCTCNCTAAN	CCCTNCGCCT	720
CGGTCGTTNC	NGGTNGCGGG	GAANGGGNAT	NNNCTCCNC	NAAGGGGGNG	AGNNNGNTAT	780
CCCCAAA						787

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TTTTTTTTTT	TTTTTTTGGC	GATGCTACTG	TTTAATTGCA	GGAGGTGGGG	GTGTGTGTAC	60
CATGTACCAG	GGCTATTAGA	AGCAAGAAGG	AAGGAGGGAG	GGCAGAGCGC	CCTGCTGAGC	120
AACAAAGGAC	TCCTGCAGCC	TTCTCTGTCT	GTCTCTTGGC	GCAGGCACAT	GGGGAGGCCT	180
CCCGCAGGGT	GGGGGCCACC	AGTCCAGGGG	TGGGAGCACT	ACANGGGGTG	GGAGTGGGTG	240
GTGGCTGGTN	CNAATGGCCT	GNCACANATC	CCTACGATTC	TTGACACCTG	GATTTACCCA	300
GGGGACCTTC	TGTTCTCCA	NGGNAACTTC	NTNNATCTCN	AAAGAACACA	ACTGTTTCTT	360
CNGCANTTCT	GGCTGTTCAT	GGAAAGCACA	GGTGTCNAT	TTNGGCTGGG	ACTTGGTACA	420
TATGGTTCCG	GCCCACCTCT	CCNCTCNAAN	AAGTAATTCA	CCCCCCCCCN	CCNTCTNTTG	480
CCTGGGCCCT	TAANTACCCA	CACCGGAACT	CANTTANTTA	TTCATCTTNG	GNTGGGCTTG	540
NTNATCNCCN	CCTGAANGCG	CCAAGTTGAA	AGGCCACGCC	GTNCCCNCTC	CCCATAGNAN	600
NTTTTNNCNT	CANCTAATGC	CCCCCNGGC	AACNATCCAA	TCCCCCCCCN	TGGGGGCCCC	660
AGCCCCANGG	CCCCGNCTCG	GGNNNCCNGN	CNCGNANTCC	CCAGGNTCTC	CCANTCNGNC	720
CCNNNGCNCC	CCCGCACGCA	GAACANAAGG	NTNGAGCCNC	CGCANNNNNN	NGGTNNCNAC	780
CTCGCCCCCC	CCNCGNNG					799

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 789 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	60
TTTNNCCNAG	GGCAGGTTTA	TTGACAACCT	CNCGGGACAC	AANCAGGCTG	GGGACAGGAC	120
GGCAACAGGC	TCCGGCGGCG	GCGGCGGCGG	CCCTACCTGC	GGTACCAAAT	NTGCAGCCTC	180
CGCTCCCCTG	TGATNTTCCT	CTGCAGCTGC	AGGATGCCNT	AAAACAGGGC	CTCGGCCNTN	240
GGTGGGCACC	CTGGGATTTN	AATTTCACG	GGCACAATGC	GGTCGCANCC	CCTCACCACC	300
NATTAGGAAT	AGTGGTNTTA	CCCNCCNCCG	TTGGCNCAC	CCCCNTGGAA	ACCAC'TNTC	360
GCGGCTCCGG	CATCTGGTCT	TAAACCTTGC	AAACNCTGGG	GCCCTCTTTT	TGGTTANTNT	420
NCCNGCCACA	ATCATNACTC	AGACTGGCNC	GGGCTGGCCC	CAAAAAANCN	CCCCAAAACC	480
GGNCCATGTC	TTNNCGGGGT	TGCTGCNATN	TNCATCACCT	CCCGGGCNCA	NCAGGNCAAC	540
CCAAAAGTTC	TTNGGGCCCN	CAAAAAANCT	CCGGGGGGNC	CCAGTTTCAA	CAAAGTCATC	600
CCCCTTGGCC	CCCAAATCCT	CCCCCGNTT	NCTGGGTTTG	GGAACCCACG	CCTCTNNCTT	660
TGGNNGGCAA	GNTGGNTCCC	CCTTCGGGCC	CCCGGTGGGC	CCNNCTCTAA	NGAAAAACNCC	720
NTCCTNNNCA	CCATCCCCCC	NNGNNACGNC	TANCAANGNA	TCCCT'TTTT	TANAAACGGG	780
CCCCCCNCG						789

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 793 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GACAGAACAT	GTTGGATGGT	GGAGCACCTT	TCTATACGAC	TTACAGGACA	GCAGATGGGG	60
AATTCATGGC	TGTTGGAGCA	ATANAACCCC	AGTTC'TACGA	GCTGCTGATC	AAAGGACTTG	120
GAATAAGTC	TGATGAACTT	CCCAATCAGA	TGAGCATGGA	TGATTGGCCA	GAAATGAANA	180
AGAAGTTTGC	AGATGTATTT	GCAAAGAAGA	CGAAGGCAGA	GTGGTGTCAA	ATCTTTGACG	240
GCACAGATGC	CTGTGTGACT	CCGGTTCTGA	CTTTTGAGGA	GGTTGTTCAT	CATGATCACA	300
ACAANGAAGC	GGGCTCGTTT	ATCACCANTG	AGGAGCAGGA	CGTGAGCCCC	CGCCCTGCAC	360
CTCTGCTGTT	AAACACCCCA	GCCATCCCTT	CTTTCAAAAG	GGATCCACTA	CTTCTAGAGC	420
GGNCGCCACC	GCGGTGGAGC	TCCAGCTTTT	GTTCCCTTTA	GTGAGGGTTA	ATTGCGCGCT	480
TGGCGTAATC	ATGGTCATAN	CTGTTTCCTG	TGTGAAATTG	TTATCCGCTC	ACAATTCCAC	540
ACAACATACG	ANCCGGAAGC	ATNAAATTTT	AAAGCCTGGN	GGTNGCCTAA	TGANTGAACT	600
NACTCACATT	AATTGGCTTT	GCGCTCACTG	CCCGCTTCC	AGTCCGGAAA	ACCTGTCCTT	660
GCCAGCTGCC	NTTAATGAAT	CNGGCCACCC	CCCGGGGAAA	AGGCNGTTTG	CTTNTTGGGG	720
CGCNCTTCCC	GCTTCTCGC	TTCCTGAANT	CCTTCCCCCC	GGTCTTTCGG	CTTGCGGCNA	780
ACGGTATCNA	CCT					793

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 756 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

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GCCGCGACCG GCATGTACGA GCAACTCAAG GCGGAGTGGA ACCGTAAAAG CCCCAATCTT      60
ANCAAGTGCG GGGGAANAGCT GGGTCGACTC AAGCTAGTTC TTCTGGAGCT CAACTTCTTG      120
CCAACCACAG GGACCAAGCT GACCAAACAG CAGCTAATTC TGGCCCGTGA CATACTGGAG      180
ATCGGGGGCC AATGGAGCAT CCTACGCAAN GACATCCCCT CCTTCGAGCG CTACATGGCC      240
CAGCTCAAAT GCTACTACTT TGATTACAAN GAGCAGCTCC CCGAGTCAGC CTATATGCAC      300
CAGCTCTTGG GCCTCAACCT CCTCTTCCTG CTGTCCCAGA ACCGGGTGGC TGANTNCCAC      360
ACGGANTTGG ANCGGCTGCC TGCCCAANGA CATAKANACC AATGTCTACA TCNACCACCA      420
GTGTCCTGGA GCAATACTGA TGGANGGCAG CTACCNCAA GTNTTCCTGG CCNAGGGTAA      480
CATCCCCCGC CGAGAGCTAC ACCTTCTTCA TTGACATCCT GCTCGACACT ATCAGGGATG      540
AAAATCGCNG GGTTGCTCCA GAAAGGCTNC AANAANATCC TTTCNCTGA AGGCCCCCGG      600
ATNCNCTAGT NCTAGAATCG GCCCGCCATC GCGGTGGANC CTCCAACCTT TCGTTNCCCT      660
TTACTGAGGG TTNATTGCCG CCCTTGGCGT TATCATGGTC ACNCCNGTTN CCTGTGTTGA      720
AATTNTTAAC CCCCCACAAT TCCACGCCNA CATNNG                                756

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(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

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GGGGATCTCT ANATCNACCT GNATGCATGG TTGTCGGTGT GGTGCTGTGC GATGAANATG      60
AACAGGATCT TGCCCTTGAA GCTCTCGGCT GCTGTNTTTA AGTTGCTCAG TCTGCCGTCA      120
TAGTCAGACA CNCTCTTGGG CAAAAACAN CAGGATNTGA GTCTTGATTT CACCTCCAAT      180
AATCTTCNGG GCTGTCTGCT CGGTGAACTC GATGACNANG GGCAGCTGGT TGTGTNTGAT      240
AAANTCCANC ANGTTCTCCT TGGTGACCTC CCCTTCAAAG TTGTCCGGC CTTCATCAAA      300
CTTCTNNAAN ANGANNANCC CANCTTTGTC GAGCTGGNAT TTGGANAACA CGTCACTGTT      360
GGAAACTGAT CCCAAATGGT ATGTCATCCA TCGCCTCTGC TGCCTGCAA AACTTGCTT      420
GGCNCAAATC CGACTCCCN TCCTTGAAAG AAGCCNATCA CACCCCCCTC CCTGGACTCC      480
NNCAANGACT CTNCCGCTNC CCCNTCCNNG CAGGGTTGGT GGCANNCCGG GCCNTGCGC      540
TTCTTCAGCC AGTTCACNAT NTTTCATCAG CCCTCTGCCA GCTGTNTAT TCCTTGGGGG      600
GGAANCCGTC TCTCCCTTCC TGAANNAACT TTGACCGTNG GAATAGCCGC GCNTCNCCNT      660
ACNTNCTGGG CCGGGTTCAA ANTCCCTCCN TTGNCNNTCN CCTCGGGCCA TTCTGGATTT      720
NCCNAACTTT TTCCTTCCCC CNCCCCNCGG NGTTTGGNTT TTTCATNGGG CCCCAACTCT      780
GCTNTTGGCC ANTCCCCTGG GGGCNTNTAN CNCCCCCTNT GGTCCCNTNG GGCC                                834

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(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CGGNCGCTTT	CCNGCCGCGC	CCCGTTTCCA	TGACNAAGGC	TCCCTTCANG	TTAAATACNN	60
CCTAGNAAAC	ATTAATGGGT	TGCTCTACTA	ATACATCATA	CNAACCAGTA	AGCCTGCCCCA	120
NAACGCCAAC	TCAGGCCATT	CCTACCAAAG	GAAGAAAGGC	TGGTCTCTCC	ACCCCTGTGA	180
GGAAAGGCCCT	GCCTTGTAAG	ACACCACAAT	NCGGCTGAAT	CTNAAGTCTT	GTGTTTTACT	240
AATGGAAAAA	AAAAATAAAC	AANAGGTTTT	GTTCTCATGG	CTGCCCACCG	CAGCCTGGCA	300
CTAAAACANC	CCAGCGCTCA	CTTCTGCTTG	GANAAATATT	CTTTGCTCTT	TTGGACATCA	360
GGCTTGATGG	TATCACTGCC	ACNTTTCAC	CCAGCTGGGC	NCCCTTCCCC	CATNTTGTGTC	420
ANTGANCTGG	AAGGCCTGAA	NCTTAGTCTC	CAAAAGTCTC	NGCCCACAAG	ACCGGCCACC	480
AGGGGANGTC	NTTNCAGTG	GATCTGCCAA	ANANTACCCN	TATCATCNNT	GAATAAAAAG	540
GCCCTGAAC	GANATGCTTC	CANCANCTT	TAAGACCCAT	AATCCTNGAA	CCATGGTGCC	600
CTTCCGGTCT	GATCCNAAAG	GAATGTTCCCT	GGGTCCCANT	CCCTCCTTTG	TNCTTACGT	660
TGTNTTGGAC	CCNTGCTNGN	ATNACCCAAN	TGANATCCCC	NGAAGCACCC	TNCCCCTGGC	720
ATTTGANTTT	CNTAAATTCT	CTGCCCTACN	NCTGAAAGCA	CNATTCCCTN	GGCNCCNAAN	780
GGNGAACTCA	AGAAGTCTN	NGAAAAACCA	CNCN			814

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 760 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GCATGCTGCT	CTTCCTCAAA	GTTGTTCTTG	TTGCCATAAC	AACCACCATA	GGTAAAGCGG	60
GCGCAGTGTT	CGCTGAAGGG	GTTGTAGTAC	CAGCGCGGGA	TGCTCTCCTT	GCAGAGTCCT	120
GTGTCTGGCA	GGTCCACGCA	ATGCCCTTTG	TCACTGGGGA	AATGGATGCG	CTGGAGCTCG	180
TCNAANCCAC	TCGTGTATTT	TTCACANGCA	GCCTCCTCCG	AAGCNTCCGG	GCAGTTGGGG	240
GTGTCGTAC	ACTCCACTAA	ACTGTGCGATN	CANCAGCCCA	TTGCTGCAGC	GGAAGTGGGT	300
GGGCTGACAG	GTGCCAGAAC	ACACTGGATN	GGCCTTTCCA	TGGAAGGGCC	TGGGGGAAAT	360
CNCCTNANCC	CAAACTGCCT	CTCAAAGGCC	ACCTTGCACA	CCCCGACAGG	CTAGAAATGC	420
ACTCTTCTTC	CCAAAGGTAG	TTGTTCTTGT	TGCCCAAGCA	NCCTCCANCA	AACCAAAANC	480
TTGCAAAATC	TGCTCCGTGG	GGGTCATNNN	TACCANGGTT	GGGGAAANAA	ACCCGGCNGN	540
GANCCNCCTT	GTTTGAATGC	NAAGGNAATA	ATCCTCCTGT	CTTGCTTGGG	TGGAANAGCA	600
CAATTGAACT	GTAAACNTTG	GGCCGNGTTC	CNCTNGGGTG	GTCTGAAACT	AATCACCGTC	660
ACTGGA AAAA	GGTANGTGCC	TTCTTGAAT	TCCCAAANTT	CCCCTNGNTT	TGGGTNNTTT	720
CTCCTCTNCC	CTAAAAATCG	TNTTCCCCCC	CCNTANGGCG			760

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 724 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTAAAAA	CCCCCTCCAT	TGAATGAAAA	60
CTTCCNAAAT	TGTCCAACCC	CCTCNCCAA	ATNNCCATTT	CCGGGGGGGG	GTTCCAAACC	120

CAAATTAATT	TTGGANTTTA	AATTAAATNT	TNATTNGGGG	AANAANCCAA	ATGTNAAGAA	180
AATTTAACCC	ATTATNAACT	TAAATNCCTN	GAAACCCNTG	GNTTCCAAAA	ATTTTAAACC	240
CTTAAATCCC	TCCGAAATTG	NTAANGGAAA	ACCAAATTCN	CCTAAGGCTN	TTTGAAGGTT	300
NGATTTAAAC	CCCCTTNANT	TNTTTTNACC	CNNGNCTNAA	NTATTTNGNT	TCCGGTGTTT	360
TCCTNTTAAN	CNTNGGTAAC	TCCCGNTAAT	GAANNNCCCT	AANCCAATTA	AACCGAATTT	420
TTTTTGAATT	GGAAATTCCN	NGGGAATTNA	CCGGGGTTTT	TCCCNTTTGG	GGGCCATNCC	480
CCCNCITTCG	GGGTTTGGGN	NTAGGTTGAA	TTTTTNNANG	NCCCCAAAAA	NCCCCCAANA	540
AAAAAACTCC	CAAGNNTTAA	TTNGAATNTC	CCCCTTCCCA	GGCCTTTTGG	GAAAGGNGGG	600
TTTNTGGGGG	CCNGGGANTT	CNTTCCCCCN	TTNCCNCCCC	CCCCCNGGT	AAANGGTTAT	660
NGNNTTTGGT	TTTTGGGCCC	CTTNANGGAC	CTTCCGGATN	GAAATTAAAT	CCCCGGGNCG	720
GCCG						724

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

TTTTTTTTTT	TTTTTCTTTG	CTCACATTTA	ATTTTATTTT	TGATTTTTTT	TAATGCTGCA	60
CAACACAATA	TTTATTTTCAT	TGTTTCTTTT	TATTTTCATTT	TATTTGTTTG	CTGCTGCTGT	120
TTTATTTAT	TTTACTGAAA	GTGAGAGGGA	ACTTTTGTGG	CCTTTTTTCC	TTTTTCTGTA	180
GGCCGCCTTA	AGCTTTCTAA	ATTTGGAACA	TCTAAGCAAG	CTGAANGGAA	AAGGGGGTTT	240
CGCAAAATCA	CTCGGGGGAA	NGGAAAGGTT	GCTTTGTAA	TCATGCCCTA	TGGTGGGTGA	300
TTAACTGCTT	GTACAATTAC	NTTTCACTTT	TAATTAATTG	TGCTNAANGC	TTTAATTANA	360
CTTGGGGGTT	CCCTCCCCAN	ACCAACCCCN	CTGACAAAAA	GTGCCNGCCC	TCAAATNATG	420
TCCCGGCNNT	CNTTGAAACA	CACNGCNGAA	NGTTCTCATT	NTCCCNCCNC	CAGGTNAAAA	480
TGAAGGGTTA	CCATNTTTAA	CNCCACCTCC	ACNTGGCNNN	GCCTGAATCC	TCNAAAANCN	540
CCCTCAANCN	AATTNCTNNG	CCCCGGTCNC	GCNTNNGTCC	CNCCCGGGCT	CCGGGAANTN	600
CACCCCNCA	ANNCNNTNNC	NAACNAAATT	CCGAAAATAT	TCCCNNTCNC	TCAATTCCCC	660
CNNAGACTNT	CCTCNNCNAN	CNCAATTTTC	TTTTNNTCAC	GAACNCGNNC	CNNAAAATGN	720
NNNNNCCTC	CNCTNGTCCN	NAATCNCCAN	C			751

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 753 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GTGGTATTTT	CTGTAAGATC	AGGTGTTCTT	CCCTCGTAGG	TTAGAGGAA	ACACCCTCAT	60
AGATGAAAAC	CCCCCGAGA	CAGCAGCACT	GCAACTGCCA	AGCAGCCGGG	GTAGGAGGGG	120
CGCCCTATGC	ACAGCTGGGC	CCTTGAGACA	GCAGGGCTTC	GATGTCAGGC	TCGATGTCAA	180
TGGTCTGGAA	GCGGCGGCTG	TACCTGCGTA	GGGGCACACC	GTCAGGGCCC	ACCAGGAACT	240
TCTCAAAGTT	CCAGGCAACN	TCGTTGCGAC	ACACCGGAGA	CCAGGTGATN	AGCTTGGGGT	300

CGGTCATAAN	CGCGGTGGCG	TCGTGCTGG	GAGCTGGCAG	GGCCTCCCGC	AGGAAGGCNA	360
ATAAAAGGTG	CGCCCCGCA	CCGTTCACT	CGCACTTCTC	NAANACCATG	ANGTTGGGCT	420
CNAACCCACC	ACCANNCCGG	ACTTCCTTGA	NGGAATTCCC	AAATCTCTTC	GNTCTTGGGC	480
TTCTNCTGAT	GCCCTANCTG	GTTGCCCNGN	ATGCCAANCA	NCCCCAANCC	CCGGGGTCCCT	540
AAANCACCCN	CCTCCTCNTT	TCATCTGGGT	TNTTNTCCCC	GGACNTGGT	TCCTCTCAAG	600
GGANCCCAT	TCTCNACCAN	TACTCACCT	NCCCCCCCNT	GNNACCCANC	CTTCTANNGN	660
TTCCCNCCCG	NCCTCTGGCC	CNTCAAANAN	GCTTNCACNA	CCTGGGTCTG	CCTTCCCCCC	720
TNCCCTATCT	GNACCCNCN	TTTGTCTCAN	TNT			753

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

ACTATATCCA	TCACAACAGA	CATGCTTCAT	CCCATAGACT	TCTTGACATA	GCTTCAAATG	60
AGTGAACCCA	TCCTTGATTT	ATATACATAT	ATGTTCTCAG	TATTTTGGGA	GCCTTTCCAC	120
TTCTTTAAAC	CTTGTTTCATT	ATGAACACTG	AAAATAGGAA	TTTGTGAAGA	GTTAAAAAGT	180
TATAGCTTGT	TTACGTAGTA	AGTTTTTGAA	GTCTACATTC	AATCCAGACA	CTTAGTTGAG	240
TGTTAAACTG	TGATTTTTAA	AAAATATCAT	TTGAGAATAT	TCTTTCAGAG	GTATTTTCAT	300
TTTTACTTTT	TGATTAATTG	TGTTTTATAT	ATTAGGGTAG	T		341

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

ACTTACTGAA	TTTAGTTCTG	TGCTCTTCCT	TATTTAGTGT	TGTATCATAA	ATACTTTGAT	60
GTTTCAAACA	TTCTAAATAA	ATAATTTTCA	GTGGCTTCAT	A		101

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

ACATCTTTGT TACAGTCTAA GATGTGTTCT TAAATCACCA TTCCTTCCTG GTCCTCACCC	60
TCCAGGGTGG TCTCACACTG TAATTAGAGC TATTGAGGAG TCTTTACAGC AAATTAAGAT	120
TCAGATGCCT TGCTAAGTCT AGAGTTCTAG AGTTATGTTT CAGAAAAGTCT AAGAAACCCA	180
CCTCTTGAGA GGTCAAGTAA GAGGACTTAA TATTTCATAT CTACAAAATG ACCACAGGAT	240
TGGATACAGA ACGAGAGTTA TCCTGGATAA CTCAGAGCTG AGTACCTGCC CGGGGGCCGC	300
TCGAA	305

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 852 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

ACATAAATAT CAGAGAAAAG TAGTCTTTGA AATATTTACG TCCAGGAGTT CTTTGTTTCT	60
GATTATTTGG TGTGTGTTTT GGTGTGTGTC CAAAGTATTG GCAGCTTCAG TTTTCATTTT	120
CTCTCCATCC TCGGGCATTG TTCCCAAATT TATATACCAG TCTTCGTCCA TCCACACGCT	180
CCAGAATTTT TCTTTTGTAG TAATATCTCA TAGCTCGGCT GAGCTTTTCA TAGGTCATGC	240
TGCTGTTGTT CTCTTTTSTA CCCCATAGCT GAGCCACTGC CTCTGATTTT AAGAACCTGA	300
AGACGCCCTC AGATCGGTCT TCCCATTTTA TTAATCCTGG GTTCTTGCTT GGGTTCAAGA	360
GGATGTCGCG GATGAATTCC CATAAGTGAG TCCCTCTCGG GTTGTGCTTT TTGGTGTGGC	420
ACTTGGCAGG GGGGTCTTGC TCCTTTTCA TATCAGGTGA CTCTGCAACA GGAAGGTGAC	480
TGGTGGTTGT CATGGAGATC TGAGCCCGGC AGAAAGTTTT GCTGTCCAAC AAATCTACTG	540
TGCTACCATA GTTGGTGTCA TATAAATAGT TCTNGTCTTT CCAGGTGTTT ATGATGGAAG	600
GCTCAGTTTG TTCAGTCTTG ACAATGACAT TGTGTGTGGA CTGGAACAGG TCACTACTGC	660
ACTGGCCGTT CCACTTCAGA TGCTGCAAGT TGCTGTAGAG GAGNTGCCCC GCCGTCCCTG	720
CCGCCCCGGT GAACTCCTGC AAACCTCATGC TGCAAAGGTG CTCGCCGTTG ATGTCGAACT	780
CNTGGAAAGG GATACAATTG GCATCCAGCT GGTGGTGTG CAGGAGGTGA TGGAGCCACT	840
CCCACACCTG GT	852

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 234 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

ACAACAGACC CTTGCTCGCT AACGACCTCA TGCTCATCAA GTTGGACGAA TCCGTGTCCG	60
AGTCTGACAC CATCCGGAGC ATCAGCATTG CTTGCGAGTG CCCTACCGCG GGGAACTCTT	120
GCCTCGTTTC TGGCTGGGGT CTGCTGGCGA ACGGCAGAAT GCCTACCGTG CTGCAGTGCG	180
TGAACGTGTC GGTGGTGTCT GAGGAGGTCT GCAGTAAGCT CTATGACCCG CTGT	234

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 590 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

ACTTTTATT TAAATGTTTA TAAGGCAGAT CTATGAGAAT GATAGAAAAC ATGGTGTGTA	60
ATTTGATAGC AATATTTTGG AGATTACAGA GTTTTAGTAA TTACCAATTA CACAGTTAAA	120
AAGAAGATAA TATATTCCAA GCANATACAA AATATCTAAT GAAAGATCAA GGCAGGAAAA	180
TGANTATAAC TAATTGACAA TGGAAAATCA ATTTTAATGT GAATTGCACA TTATCCTTTA	240
AAAGCTTTCA AAANAAANAA TTATTGCAGT CTANTTAATT CAAACAGTGT TAAATGGTAT	300
CAGGATAAAN AACTGAAGGG CANAAAGAAT TAATTTTCAC TTCATGTAAC NCACCCANAT	360
TTACAATGGC TTAAATGCAN GGAAAAAGCA GTGGAAGTAG GGAAGTANTC AAGGTCTTTC	420
TGGTCTCTAA TCTGCCTTAC TCTTTGGGTG TGGCTTTGAT CCTCTGGAGA CAGCTGCCAG	480
GGCTCCTGTT ATATCCACAA TCCCAGCAGC AAGATGAAGG GATGAAAAAG GACACATGCT	540
GCCTTCCTTT GAGGAGACTT CATCTCACTG GCCAACACTC AGTCACATGT	590

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 774 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

ACAAGGGGGC ATAATGAAGG AGTGGGGANA GATTTTAAAG AAGGAAAAAA AACGAGGCC	60
TGAACAGAAT TTTCTGNAC AACGGGGCTT CAAAATAATT TTCTTGGGA GGTCAAGAC	120

GCTTCACTGC	TTGAAACTTA	AATGGATGTG	GGACANAATT	TTCTGTAATG	ACCCTGAGGG	180
CATTACAGAC	GGGACTCTGG	GAGGAAGGAT	AAACAGAAAG	GGGACAAAGG	CTAATCCCAA	240
AACATCAAAG	AAAGGAAGGT	GGCGTCATAC	CTCCAGCCT	ACACAGTTCT	CCAGGGCTCT	300
CCTCATCCCT	GGAGGACGAC	AGTGGAGGAA	CAACTGACCA	TGTCCCAGG	CTCCTGTGTG	360
CTGGCTCCTG	GTCTTCAGCC	CCCAGCTCTG	GAAGCCCACC	CTCTGCTGAT	CCTGCGTGGC	420
CCACACTCCT	TGAACACACA	TCCCCAGGTT	ATATTCTCTG	ACATGGCTGA	ACCTCCTATT	480
CCTACTTCCG	AGATGCCTTG	CTCCCTGCAG	CCTGTCAAAA	TCCCACTCAC	CCTCCAAACC	540
ACGGCATGGG	AAGCCTTTCT	GACTTGCCTG	ATTACTCCAG	CATCTTGGAA	CAATCCCTGA	600
TTCCCCACTC	CTTAGAGGCA	AGATAGGGTG	GTTAAGAGTA	GGGCTGGACC	ACTTGGAGCC	660
AGGCTGCTGG	CTTCAAATTN	TGGCTCATTT	ACGAGCTATG	GGACCTTGGG	CAAGTNATCT	720
TCACTTCTAT	GGGCNTCATT	TTGTTCTACC	TGCAAAATGG	GGGATAATAA	TAGT	774

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CANAAATTGA	AATTTTATAA	AAAGGCATTT	TTCTCTTATA	TCCATAAAAT	GATATAATTT	60
TTGCAANTAT	ANAAATGTGT	CATAAATTAT	AATGTTCTT	AATTACAGCT	CAACGCAACT	120
TGGT						124

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GCCGATGCTA	CTATTTTATT	GCAGGAGGTG	GGGGTGTTTT	TATTATTCTC	TCAACAGCTT	60
TGTGGCTACA	GGTGGTGTCT	GACTGCATNA	AAAANTTTTT	TACGGGTGAT	TGCAAAAATT	120
TTAGGGCACC	CATATCCCAA	GCANTGT				147

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

ACATTAAATT AATAAAAGGA CTGTTGGGGT TCTGCTAAAA CACATGGCTT GATATATTGC	60
ATGTTTGTAG GTTAGGAGGA GTTAGGCATA TGTTTTGGGA GAGGGGT	107

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 204 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GTCCTAGGAA GTCTAGGGGA CACACGACTC TGGGGTCACG GGGCCGACAC ACTTGCACGG	60
CGGGAAGGAA AGGCAGAGAA GTGACACCGT CAGGGGGAAA TGACAGAAAG GAAAATCAAG	120
GCCTTGCAAG GTCAGAAAGG GGACTCAGGG CTTCCACCAC AGCCCTGCCC CACTTGGCCA	180
CCTCCCTTTT GGGACCAGCA ATGT	204

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 491 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

ACAAAGATAA CATTTATCTT ATAACAAAAA TTTGATAGTT TTAAAGGTTA GTATTGTGTA	60
GGGTATTTTC CAAAAGACTA AAGAGATAAC TCAGGTAAAA AGTTAGAAAT GTATAAAACA	120
CCATCAGACA GGTTTTTTAA AAACAACATA TTACAAAATT AGACAATCAT CCTTAAAAAA	180
AAAACCTCTT GTATCAATTT CTTTGTTC AATGACTGA CTTAANTATT TTTAAATATT	240
TCANAAACAC TTCCTCAAAA ATTTTCAANA TGGTAGCTTT CANATGTNCC CTCAGTCCCA	300
ATGTTGCTCA GATAAATAAA TCTCGTGAGA ACTTACCACC CACCACAAGC TTTCTGGGGC	360
ATGCAACAGT GTCTTTTCTT TNCTTTTCT TTTTTTTTTT TTACAGGCAC AGAAACTCAT	420

CAATTTTATT TGGATAACAA AGGGTCTCCA AATTATATTG AAAAATAAAT CCAAGTTAAT 480
ATCACTCTTG T 491

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 484 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

ACATAATTTA GCAGGGCTAA TTACCATAAG ATGCTATTTA TTAANAGGTN TATGATCTGA 60
 GTATTAACAG TTGCTGAAGT TTGGTATTTT TATGCAGCAT TTTCTTTTGT CTTTGATAAC 120
 ACTACAGAAC CCTTAAGGAC ACTGAAAATT AGTAAAGTAAA GTTCAGAAAC ATTAGCTGCT 180
 CAATCAAATC TCTACATAAC ACTATAGTAA TTAAAACGTT AAAAAAAGT GTTGAAATCT 240
 GCACTAGTAT ANACCGCTCC TGTCAGGATA ANACTGCTTT GGAACAGAAA GGGAAAAANC 300
 AGCTTTGANT TTCTTTGTGC TGATANGAGG AAAGGCTGAA TTACCTTGTT GCCTCTCCCT 360
 AATGATTGGC AGGTCNGGTA AATNCCAAAA CATATTCCAA CTCAACACTT CTTTTCCNCG 420
 TANCTTGANT CTGTGTATTC CAGGANCAGG CGGATGGAAT GGGCCAGCCC NCGGATGTTC 480
 CANT 484

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 151 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

ACTAAACCTC GTGCTTGGA ACTCCATACA GAAAACGGTG CCATCCCTGA ACACGGCTGG 60
 CCACTGGGTA TACTGCTGAC AACCACAACA AAAAAACAC AAATCCTTGG CACTGGCTAG 120
 TCTATGTCCT CTCAAGTGCC TTTTGTGTTG T 151

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 91 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

60

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

ACCTGGCTTG TCTCCGGGTG GTTCCCGGCG CCCCCACGG TCCCCAGAAC GGACACTTTC	60
GCCCTCCAGT GGATACTCGA GCCAAAGTGG T	91

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 133 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GGCGGATGTG CGTTGGTTAT ATACAAATAT GTCATTTTAT GTAAGGGACT TGAGTATACT	60
TGGATTTTGT GTATCTGTGG GTTGGGGGGA CGTCCAGGA ACCAATACCC CATGGATACC	120
AAGGGACAAC TGT	133

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 147 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

ACTCTGGAGA ACCTGAGCCG CTGCTCCGCC TCTGGGATGA GGTGATGCAN GCNGTGGCGC	60
GACTGGGAGC TGAGCCCTTC CCTTTGCGCC TGCCTCAGAG GATTGTTGCC GACNTGCANA	120
TCTCANTGGG CTGGATNCAT GCAGGGT	147

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 198 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

ACAGGGATAT AGGTTTNAAG TTATTGTNAT TGAAAAATAC ATTGAATTTT CTGTATACTC	60
TGATTACATA CATTTATCCT TAAAAAAGA TGAAATCTT AATTTTATG CCATCTATTA	120
ATTTACCAAT GAGTTACCTT GTAAATGAGA AGTCATGATA GCACTGAATT TTAAC TAGTT	180
TTGACTTCTA AGTTTGGT	198

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 330 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

ACAACAAATG GGTGTGAGG AAGTCTTATC AGCAAACTG GTGATGGCTA CTGAAAAGAT	60
CCATTGAAAA TTATCATTAA TGATTTTAAA TGACAAGTTA TCAAAACTC ACTCAATTTT	120
CACCTGTGCT AGCTTGCTAA AATGGGAGTT AACTCTAGAG CAAATATAGT ATCTTCTGAA	180
TACAGTCAAT AAATGACAAA GCCAGGGCCT ACAGGTGGTT TCCAGACTTT CCAGACCCAG	240
CAGAAGGAAT CTATTTTATC ACATGGATCT CCGTCTGTGC TCAAATACC TAATGATATT	300
TTTCGTCTTT ATTGGACTTC TTTGAAGAGT	330

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 175 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

ACCGTGGGTG CCTTCTACAT TCCTGACGGC TCCTTCACCA ACATCTGGTT CTACTTCGGC	60
GTCGTGGGCT CCTTCCTCTT CATCCTCATC CAGCTGGTGC TGCTCATCGA CTTTGCGCAC	120
TCCTGGAACC AGCGGTGGCT GGGCAAGGCC GAGGAGTGCG ATTCCCGTGC CTGGT	175

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

ACCCCACTTT TCCTCCTGTG AGCAGTCTGG ACTTCTCACT GCTACATGAT GAGGGTGAGT	60
GGTTGTTGCT CTTCAACAGT ATCTCCCCCT TTCCGGATCT GCTGAGCCGG ACAGCAGTGC	120
TGGACTGCAC AGCCCCGGGG CTCCACATTG CTGT	154

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

CGCTCGAGCC CTATAGTGAG TCGTATTAGA	30
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(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

ACAAGTCATT TCAGCACCTT TTGCTCTTCA AACTGACCA TCTTTTATAT TTAATGCTTC	60
CTGTATGAAT AAAAATGGTT ATGTCAAGT	89

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 97 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

ACCGGAGTAA CTGAGTCGGG ACGCTGAATC TGAATCCACC AATAAATAAA GGTTCGTCAG	60
AATCAGTGCA TCCAGGATTG GTCCTTGGAT CTGGGGT	97

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 377 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

ACAACAANAA NTCCCTTCTT TAGGCCACTG ATGGAAACCT GGAACCCCTT TTTGATGGCA	60
GCATGGCGTC CTAGGCCTTG ACACAGCGGC TGGGGTTTGG GCTNTCCCAA ACCGCACACC	120
CCAACCCTGG TCTACCCACA NTTCTGGCTA TGGGCTGTCT CTGCCACTGA ACATCAGGGT	180
TCGGTCATAA NATGAAATCC CAANGGGGAC AGAGGTCAGT AGAGGAAGCT CAATGAGAAA	240
GGTGCTGTTT GCTCAGCCAG AAAACAGCTG CCTGGCATTG GCCGCTGAAC TATGAACCCG	300
TGGGGGTGAA CTACCCCAN GAGGAATCAT GCCTGGGCGA TGCAANGGTG CCAACAGGAG	360
GGGCGGGAGG AGCATGT	377

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 305 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

ACGCCTTTCC CTCAGAATTC AGGGAAGAGA CTGTCGCCTG CCTTCCTCCG TTGTTGCGTG	60
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AGAACCCGTG	TGCCCCCTTC	CACCATATCC	ACCCTCGCTC	CATCTTTGAA	CTCAAACACG	120
AGGAACCTAAC	TGCACCCTGG	TCCTCTCCCC	AGTCCCCAGT	TCACCCTCCA	TCCCTCACCT	180
TCCTCCACTC	TAAGGGATAT	CAACACTGCC	CAGCACAGGG	GCCCTGAATT	TATGTGGTTT	240
TTATATATTT	TTAATAAGA	TGCACTTTAT	GTCAATTTTT	AATAAAGTCT	GAAGAATTAC	300
TGTTT						305

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 385 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

ACTACACACA	CTCCACTTGC	CCTTGTGAGA	CACTTTGTCC	CAGCACTTTA	GGAATGCTGA	60
GGTCGGACCA	GCCACATCTC	ATGTGCAAGA	TTGCCCAGCA	GACATCAGGT	CTGAGAGTTC	120
CCCTTTTAAA	AAAGGGGACT	TGCTTAAAAA	AGAAGTCTAG	CCACGATTGT	GTAGAGCAGC	180
TGTGCTGTGC	TGGAGATTCA	CTTTTGAGAG	AGTTCTCCTC	TGAGACCTGA	TCTTTAGAGG	240
CTGGGCAGTC	TTGCACATGA	GATGGGGCTG	GTCTGATCTC	AGCACTCCTT	AGTCTGCTTG	300
CCTCTCCCAG	GGCCCCAGCC	TGGCCACACC	TGCTTACAGG	GCACTCTCAG	ATGCCCATAC	360
CATAGTTTCT	GTGCTAGTGG	ACCGT				385

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

ACTTAACCAG	ATATATTTTT	ACCCCAGATG	GGGATATTCT	TTGTAAAAAA	TGAAAATAAA	60
GTTTTTTTAA	TGG					73

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 536 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

ACTAGTCCAG TGTGGTGGAA TTCCATTGTG TTGGGGGCTC TCACCCTCCT CTCCTGCAGC	60
TCCAGCTTTG TGCTCTGCCT CTGAGGAGAC CATGGCCCAG CATCTGAGTA CCCTGCTGCT	120
CCTGCTGGCC ACCCTAGCTG TGGCCCTGGC CTGGAGCCCC AAGGAGGAGG ATAGGATAAT	180
CCCGGGTGGC ATCTATAACG CAGACCTCAA TGATGAGTGG GTACAGCGTG CCCTTCACTT	240
CGCCATCAGC GAGTATAACA AGGCCACCAA AGATGACTAC TACAGACGTC CGCTGCGGGT	300
ACTAAGAGCC AGGCAACAGA CCGTTGGGGG GGTGAATTAC TTCTTCGACG TAGAGGTGGG	360
CCGAACCATA TGTACCAAGT CCCAGCCCAA CTTGGACACC TGTGCCTTCC ATGAACAGCC	420
AGAACTGCAG AAGAAACAGT TGTGCTCTTT CGAGATCTAC GAAGTTCCCT GGGGAGAACA	480
GAANGTCCCT GGGTGAATC CAGGTGTCAA GAAATCCTAN GGATCTGTTG CCAGGC	536

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 477 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

ATGACCCCTA ACAGGGGCCC TCTCAGCCCT CCTAATGACC TCCGGCCTAG CCATGTGATT	60
TCACTTCCAC TCCATAACGC TCCTCATACT AGGCCTACTA ACCAACACAC TAACCATATA	120
CCAATGATGG CGCGATGTAA CACGAGAAAG CACATACCAA GGCCACCACA CACCACCTGT	180
CCAAAAAGGC CTTGATACG GGATAATCCT ATTTATTACC TCAGAAGTTT TTTTCTTCGC	240
AGGGATTTT CTGAGCCTTT TACCACTCCA GCCTAGCCCC TACCCCCCAA CTAGGAGGGC	300
ACTGGCCCC AACAGGCATC ACCCGCTAA ATCCCCTAGA AGTCCCACTC CTAAACACAT	360
CCGTATTACT CGCATCAGGA GTATCAATCA CCTGAGCTCA CCATAGTCTA ATAGAAAACA	420
ACCGAAACCA AATTATTCAA AGCACTGCTT ATTACAATTT TACTGGGTCT CTATTTT	477

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 533 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

AGAGCTATAG	GTACAGTGTG	ATCTCAGCTT	TGCAAACACA	TTTTCTACAT	AGATAGTACT	60
AGGTATTAAT	AGATATGTAA	AGAAAGAAAT	CACACCATTA	ATAATGGTAA	GATTGGTTTA	120
TGTGATTTTA	GTGGTATTTT	TGCGACCCTT	ATATATGTTT	TCCAAACTTT	CAGCAGTGAT	180
ATTATTTCCA	TAACTTAAAA	AGTGAGTTTG	AAAAAGAAAA	TCTCCAGCAA	GCATCTCATT	240
TAAATAAAGG	TTGTGCATCT	TTAAAAATAC	AGCAATATGT	GACTTTTTTA	AAAAGCTGTC	300
AAATAGGTGT	GACCCTACTA	ATAATTATTA	GAAATACATT	TAAAAACATC	GAGTACCTCA	360
AGTCAGTTTG	CCTTGAAAAA	TATCAAATAT	AACTCTTAGA	GAAATGTACA	TAAAAGAATG	420
CTTCGTAATT	TTGGAGTANG	AGGTTCCCTC	CTCAATTTTG	TATTTTAA	AAGTACATGG	480
TAAAAA	AATTCACAAC	AGTATATAAG	GCTGTAAAT	GAAGAATTCT	GCC	533

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 511 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

TATTACGGAA	AAACACACCA	CATAATTCAA	CTANCAAAGA	ANACTGCTTC	AGGGCGTGTA	60
AAATGAAAGG	CTTCCAGGCA	GTTATCTGAT	TAAAGAACAC	TAAAAGAGGG	ACAAGGCTAA	120
AAGCCGCAGG	ATGTCTACAC	TATANCAGGC	GCTATTTGGG	TTGGCTGGAG	GAGCTGTGGA	180
AAACATGGAN	AGATTGGTGC	TGGANATCGC	CGTGGCTATT	CCTCATTGTT	ATTACANAGT	240
GAGGTTCTCT	GTGTGCCCC	TGGTTTGAAA	ACCGTTCTNC	AATAATGATA	GAATAGTACA	300
CACATGAGAA	CTGAAATGGC	CCAAACCCAG	AAAGAAAGCC	CAACTAGATC	CTCAGANAC	360
GCTTCTAGGG	ACAATAACCG	ATGAAGAAAA	GATGGCCTCC	TTGTGCCCCC	GTCTGTTATG	420
ATTTCTCTCC	ATTGCAGCNA	NAAACCCGTT	CTTCTAAGCA	AACNCAGGTG	ATGATGGCNA	480
AAATACACCC	CCTCTTGAAG	NACCNCGGAGG	A			511

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 499 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

CAGTGCCAGC	ACTGGTGCCA	GTACCAGTAC	CAATAACAGT	GCCAGTGCCA	GTGCCAGCAC	60
CAGTGGTGGC	TTCACTGCTG	GTGCCAGCCT	GACCGCCACT	CTCACATTTG	GGCTCTTCGC	120
TGGCCTTGGT	GGAGCTGGTG	CCAGCACCAG	TGGCAGCTCT	GGTGCCTGTG	GTTTCTCCTA	180
CAAGTGAGAT	TTAGATATT	GTAAATCCTG	CCAGTCTTTT	TCTTCAAGCC	AGGGTGCATC	240

CTCAGAAACC	TACTCAACAC	AGCACTCTAG	GCAGCCACTA	TCAATCAATT	GAAGTTGACA	300
CTCTGCATTA	AATCTATTG	CCATTTCTGA	AAAAAAAAAA	AAAAAAGGG	CGGCCGCTCG	360
ANTCTAGAGG	GCCCGTTTAA	ACCCGCTGAT	CAGCCTCGAC	TGTGCCTTCT	ANTTGCCAGC	420
CATCTGTTGT	TTGCCCTCC	CCCNTGCCT	TCCTTGACCC	TGGAAAGTGC	CACTCCCACT	480
GTCCTTTCCT	AANTAAAAT					499

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 537 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

TTTCATAGGA	GAACACACTG	AGGAGATACT	TGAAGAATTT	GGATTCAGCC	GCGAAGAGAT	60
TTATCAGCTT	AACTCAGATA	AAATCATTGA	AAGTAATAAG	GTAAAAGCTA	GTCTCTAACT	120
TCCAGGCCCA	CGGCTCAAGT	GAATTTGAAT	ACTGCATTTA	CAGTGTAGAG	TAACACATAA	180
CATTGTATGC	ATGGAACAT	GGAGGAACAG	TATTACAGTG	TCCTACCACT	CTAATCAAGA	240
AAAGAATTAC	AGACTCTGAT	TCTACAGTGA	TGATTGAATT	CTAAAAATGG	TAATCATTAG	300
GGCTTTTGAT	TTATAANACT	TTGGGTACTT	ATACTAAATT	ATGGTAGTTA	TACTGCCTTC	360
CAGTTTGCTT	GATATATTTG	TTGATATTAA	GATTCTTGAC	TTATATTTTG	AATGGGTTCT	420
ACTGAAAAAN	GAATGATATA	TTCTTGAAGA	CATCGATATA	CATTTATTTA	CACTCTTGAT	480
TCTACAATGT	AGAAAATGAA	GGAAATGCCC	CAAATTGTAT	GGTGATAAAA	GTCCCGT	537

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

CAAANACAAT	TGTTCAAAAG	ATGCAAATGA	TACACTACTG	CTGCAGCTCA	CAAACACCTC	60
TGCATATTAC	ACGTACCTCC	TCCTGCTCCT	CAAGTAGTGT	GGTCTATTTT	GCCATCATCA	120
CCTGCTGTCT	GCTTAGAAGA	ACGGCTTTCT	GCTGCAANGG	AGAGAAATCA	TAACAGACGG	180
TGGCACAAGG	AGGCCATCTT	TTCTCATCG	GTTATTGTCC	CTAGAAGCGT	CTTCTGAGGA	240
TCTAGTTGGG	CTTTCTTTCT	GGGTTTGGGC	CATTTTCANTT	CTCATGTGTG	TACTATTCTA	300
TCATTATTGT	ATAACGGTTT	TCAAACNNGT	GGGCACNCAG	AGAACCTCAC	TCTGTAATAA	360
CAATGAGGAA	TAGCCACGGT	GATCTCCAGC	ACCAAATCTC	TCCATGTTNT	TCCAGAGCTC	420
CTCCAGCCAA	CCCAAATAGC	CGCTGCTATN	GTGTAGAACA	TCCCTGN		467

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

AAGCTGACAG CATTCTGGGCC GAGATGTCTC GCTCCGTGGC CTTAGCTGTG CTCGCGCTAC	60
TCTCTCTTTC TGGCCTGGAG GCTATCCAGC GTACTCCAAA GATTCAGGTT TACTCACGTC	120
ATCCAGCAGA GAATGGAAAG TCAAATTTCC TGAATTGCTA TGTGTCTGGG TTTCATCCAT	180
CCGACATTGA AGTTGACTTA CTGAAGAATG GAGAGAGAAT TGAAAAAGTG GAGCATTTCAG	240
ACTTGTCTTT CAGCAAGGAC TGGTCTTTCT ATCTCTTGTA CTACACTGAA TTCACCCCCA	300
CTGAAAAAGA TGAGTATGCC TGCCGTGTGA ACCATGTGAC TTTGTCACAG CCCAAGATNG	360
TTNAGTGGGA TCGANACATG TAAGCAGCAN CATGGGAGGT	400

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

CTGGAGTGCC TTGGTGTTTC AAGCCCCTGC AGGAAGCAGA ATGCACCTTC TGAGGCACCT	60
CCAGCTGCCC CGGCGGGGGA TGCGAGGCTC GGAGCACCTT TGCCCGGCTG TGATTGCTGC	120
CAGGCACTGT TCATCTCAGC TTTTCTGTCC CTTTGCTCCC GGCAAGCGCT TCTGCTGAAA	180
GTTTCATATCT GGAGCCTGAT GTCTTAACGA ATAAAGGTCC CATGCTCCAC CCGAAAAAAA	240
AAAAAAA	248

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

ACTAGTCCAG	TGTGGTGGAA	TTCCATTGTG	TTGGGCCCAA	CACAATGGCT	ACCTTTAACA	60
TCACCCAGAC	CCCGCCCTGC	CCGTGCCCCA	CGCTGCTGCT	AACGACAGTA	TGATGCTTAC	120
TCTGCTACTC	GGAAACTATT	TTTATGTAAT	TAATGTATGC	TTTCTTGTTT	ATAAATGCCT	180
GATTTAAAAA	AAAAAAAAAA	A				201

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 552 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

TCCTTTTGTT	AGGTTTTTGA	GACAACCCTA	GACCTAAACT	GTGTCACAGA	CTTCTGAATG	60
TTTAGGCAGT	GCTAGTAATT	TCCTCGTAAT	GATTCTGTTA	TTACTTTCCT	ATTCTTTATT	120
CCTCTTTCTT	CTGAAGATTA	ATGAAGTTGA	AAATTGAGGT	GGATAAATAC	AAAAAGGTAG	180
TGTGATAGTA	TAAGTATCTA	AGTGCAGATG	AAAGTGTGTT	ATATATATCC	ATTCAAAATT	240
ATGCAAGTTA	GTAATTACTC	AGGGTTAACT	AAATTACTTT	AATATGCTGT	TGAACCTACT	300
CTGTTCCCTG	GCTAGAAAAA	ATTATAAACA	GGACTTTGTT	AGTTTGGGAA	GCCAAATTGA	360
TAATATTCTA	TGTTCTAAAA	GTTGGGCTAT	ACATAAANTA	TNAAGAAATA	TGGAATTTTA	420
TTCCCAGGAA	TATGGGGTTC	ATTTATGAAT	ANTACCCGGG	ANAGAAGTTT	TGANTNAAAC	480
CNGTTTTGGT	TAATACGTTA	ATATGTCCTN	AATNAACAAG	GCNTGACTTA	TTTCCAAAAA	540
AAAAAAAAAA	AA					552

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

ACAGGGATT	GAGATGCTAA	GGCCCCAGAG	ATCGTTTGAT	CCAACCCTCT	TATTTTCAGA	60
GGGGAAAATG	GGGCTAGAA	GTTACAGAGC	ATCTAGCTGG	TGCGCTGGCA	CCCCTGCCT	120
CACACAGACT	CCCGAGTAGC	TGGGACTACA	GGCACACAGT	CACTGAAGCA	GGCCCTGTTT	180
GCAATTCACG	TTGCCACCTC	CAACTTAAAC	ATTCTTCATA	TGTGATGTCC	TTAGTCACTA	240
AGGTAAACT	TTCCCACCCA	GAAAAGGCAA	CTTAGATAAA	ATCTTAGAGT	ACTTTCATAC	300

TCTTCTAAGT CCTCTTCCAG CCTCACTTTG AGTCCTCCTT GGGGGTTGAT AGGAANTNTC	360
TCTTGGCCTTT CTCAATAAAA TCTCTATCCA TCTCATGTTT AATTGGGTAC GCNTAAAAAT	420
GCTGAAAAAA TTAAATGTT CTGGTTTCNC TTAAAAAAA AAAAAAAAAA AAAAAA	476

(2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 232 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

TTTTTTTTTG TATGCCNTCN CTGTGGNGTT ATTGTTGCTG CCACCCTGGA GGAGCCCAGT	60
TTCTTCTGTA TCTTTCTTTT CTGGGGGATC TTCCTGGCTC TGCCCCCTCCA TTCCCAGCCT	120
CTCATCCCCA TCTTGCACTT TTGCTAGGGT TGGAGGCGCT TTCCTGGTAG CCCCTCAGAG	180
ACTCAGTCAG CGGGAATAAG TCCTAGGGGT GGGGGGTGTG GCAAGCCGGC CT	232

(2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 383 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

AGGCGGGAGC AGAAGCTAAA GCCAAAGCCC AAGAAGAGTG GCAGTGCCAG CACTGGTGCC	60
AGTACCAGTA CCAATAACAT GCCAGTGCCA GTGCCAGCAC CAGTGGTGGC TTCAGTGCTG	120
GTGCCAGCCT GACCGCCACT CTCACATTG GGCTCTTCGC TGGCCTTGGT GGAGCTGGTG	180
CCAGCACCAG TGGCAGCTCT GGTGCCTGTG GTTCTCCTA CAAGTGAGAT TTAGATATT	240
GTTAATCCTG CCAGTCTTTC TCTTCAAGCC AGGGTGCATC CTCAGAAACC TACTCAACAC	300
AGCACTCTNG GCAGCCACTA TCAATCAATT GAAGTTGACA CTCTGCATTA AATCTATTTG	360
CCATTTCAAA AAAAAAAAAA AAA	383

(2) INFORMATION FOR SEQ ID NO:83:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 494 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

ACCGAATTGG	GACCGCTGGC	TTATAAGCGA	TCATGTCCTC	CAGTATTACC	TCAACGAGCA	60
GGGAGATCGA	GTCTATACGC	TGAAGAAATT	TGACCCGATG	GGACAACAGA	CCTGCTCAGC	120
CCATCCTGCT	CGGTTCTCCC	CAGATGACAA	ATACTCTCGA	CACCGAATCA	CCATCAAGAA	180
ACGCTTCAAG	GTGCTCATGA	CCCAGCAACC	GCGCCCTGTC	CTCTGAGGGT	CCTTAAACTG	240
ATGTCTTTTC	TGCCACCTGT	TACCCCTCGG	AGACTCCGTA	ACCAAACCTCT	TCGGACTGTG	300
AGCCCTGATG	CCTTTTGGCC	AGCCATACTC	TTTGGCNTCC	AGTCTCTCGT	GGCGATTGAT	360
TATGCTTGTG	TGAGGCAATC	ATGGTGGCAT	CACCCATNAA	GGGAACACAT	TTGANTTTTT	420
TTTCNCATAT	TTTAAATTAC	NACCAGAATA	NTTCAGAATA	AATGAATTGA	AAAACCTCTTA	480
AAAAAAAAAA	AAAA					494

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 380 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

GCTGGTAGCC	TATGGCGTGG	CCACGGANGG	GCTCCTGAGG	CACGGGACAG	TGACTTCCCA	60
AGTATCCTGC	GCCGCGTCTT	CTACCGTCCC	TACCTGCAGA	TCTTCGGGCA	GATTCCCCAG	120
GAGGACATGG	ACGTGGCCCT	CATGGAGCAC	AGCAACTGCT	CGTCGGAGCC	CGGCTTCTGG	180
GCACACCCTC	CTGGGGCCCA	GGCGGGCACC	TGCGTCTCCC	AGTATGCCAA	CTGGCTGGTG	240
GTGCTGCTCC	TCGTATCTTT	CCTGCTCGTG	GCCAACATCC	TGCTGGTCAC	TTGCTCATTG	300
CCATGTTCAG	TTACACATTC	GGCAAAGTAC	AGGCAACAG	CNATCTCTAC	TGGGAAGGCC	360
AGCGTTNCCG	CCTCATCCGG					380

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 481 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

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GAGTTAGCTC CTCCACAACC TTGATGAGGT CGTCTGCAGT GGCCTCTCGC TTCATACCGC      60
TNCCATCGTC ATACTGTAGG TTTGCCACCA CCTCCTGCAT CTTGGGGCGG CTAATATCCA      120
GGAAACTCTC AATCAAGTCA CCGTCNATNA AACCTGTGGC TGGTCTGTG TTCCGCTCGG      180
TGTGAAAGGA TCTCCAGAAG GAGTGCTCGA TCTTCCCCAC ACTTTTGATG ACTTTATTGA      240
GTCGATTCTG CATGTCCAGC AGGAGGTTGT ACCAGCTCTC TGACAGTGAG GTCACCAGCC      300
CTATCATGCC NTTGAACGTG CCGAAGAACA CCGAGCCTTG TGTGGGGGGT GNAGTCTCAC      360
CCGATTCTG CATTACCAGA NAGCCGTGGC AAAAGANATT GACAACTCGC CCAGGNGGAA      420
AAAGAACACC TCCTGGAAGT GCTNGCCGCT CCTCGTCCNT TGGTGGNNGC GCNTNCCTTT      480
T                                                                                   481

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(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 472 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

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AACATCTTCC TGTATAATGC TGTGTAATAT CGATCCGATN TTGTCTGCTG AGAATTCATT      60
ACTTGAAAAA GCAACTTNAA GCCTGGACAC TGGTATTAAA ATTCACAATA TGCAACACTT      120
TAAACAGTGT GTCAATCTGC TCCCTTACTT TGTCATCACC AGTCTGGGAA TAAGGGTATG      180
CCCTATTTCAC ACCTGTTAAA AGGGCGCTAA GCATTTTTGA TTCAACATCT TTTTTTTTGA      240
CACAAGTCCG AAAAAAGCAA AAGTAAACAG TTNTTAATTT GTTAGCCAAT TCACTTTCTT      300
CATGGGACAG AGCCATTTGA TTTAAAAAGC AAATGTCATA ATATTGAGCT TTGGGAGCTG      360
ATATNTGAGC GGAAGANTAG CCTTTCTACT TCACCAGACA CAACTCCTTT CATATTGGGA      420
TGTTNACNAA AGTTATGTCT CTTACAGATG GGATGCTTTT GTGGCAATTC TG                   472

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(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 413 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

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AGAAACCAGT ATCTCTNAAA ACAACCTCTC ATACCTTGTT GACCTAATTT TGTGTGCGTG      60
TGTGTGTGCG CGCATATTAT ATAGACAGGC ACATCTTTTT TACTTTTGTA AAAGCTTATG      120
CCTCTTTGGT ATCTATATCT GTGAAAGTTT TAATGATCTG CCATAATGTC TTGGGGACCT      180
TTGTCTTCTG TGTAATGGT ACTAGAGAAA ACACCTATNT TATGAGTCAA TCTAGTTNGT      240
TTTATTGAC ATGAAGGAAA TTTCCAGATN ACAACTCTNA CAACTCTCC CTTGACTAGG      300
GGGGACAAAG AAAAGCANAA CTGAACATNA GAAACAATTN CCTGGTGAGA AATTNCATAA      360

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ACAGAAATTG GGTNGTATAT TGAAANANNG CATCATTNAA ACGTTTTTTT TTT

413

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 448 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

CGCAGCGGGT CCTCTCTATC TAGCTCCAGC CTCTCGCCTG CCCCACTCCC CGCGTCCCGC	60
GTCCTAGCCN ACCATGGCCG GGCCCTGCG CGCCCGCTG CTCCTGCTGG CCATCCTGGC	120
CGTGGCCCTG GCCGTGAGCC CCGCGGCCGG CTCCAGTCCC GGCAAGCCGC CGCGCCTGGT	180
GGGAGGCCCA TGGACCCCGC GTGGAAGAAG AAGGTGTGCG GCGTGCACTG GACTTTGCCG	240
TCGGCNANTA CAACAAACCC GCAACNACTT TTACCNAGCN CGCGCTGCAG GTTGTGCCGC	300
CCCAANCAAA TTGTTACTNG GGGTAANTAA TTCTTGGAAG TTGAACCTGG GCCAAACNNG	360
TTTACCAGAA CCNAGCCAAT TNGAACAATT NCCCCTCCAT AACAGCCCCT TTTAAAAAGG	420
GAANCANTCC TGNICTTTTC CAAATTTT	448

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

GAATTTTGTG CACTGGCCAC TGTGATGGAA CCATTGGGCC AGGATGCTTT GAGTTTATCA	60
GTAGTGATTC TGCCAAAGTT GGTGTTGTAA CATGAGTATG TAAATGTCA AAAAATTAGC	120
AGAGGTCTAG GTCTGCATAT CAGCAGACAG TTTGTCCGTG TATTTGTAG CTTTGAAGTT	180
CTCAGTGACA AGTTNNTTCT GATGCGAAGT TCTNATTCCA GTGTTTGTAG CTTTGCATC	240
TTTATGTTN AGACTTGCCT CTNTNAAATT GCTTTGTNT TCTGCAGGTA CTATCTGTGG	300
TTTAACAAAA TAGAANNACT TCTCTGCTTN GAANATTGA ATATCTTACA TCTNAAAATN	360
AATCTCTCC CCATANNAAA ACCCANGCCC TTGGGANAAT TTGAAAAANG GNTCCTTCNN	420
AATTCNNANA ANTTCAGNTN TCATACAACA NAACNGGANC CCC	463

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

AGGGATTGAA	GGTCTNTTNT	ACTGTCTGGAC	TGTTTCAATCA	CCAACTCTAC	AAGTTGCTGT	60
CTTCCACTCA	CTGTCTGTAA	GCNTNTTAAAC	CCAGACTGTA	TCTTCATAAA	TAGAACAAAT	120
TCTTCACCAG	TCACATCTTC	TAGGACCTTT	TTGGATTTCAG	TTAGTATAAG	CTCTTCCACT	180
TCCTTTGTTA	AGACTTCATC	TGGTAAAGTC	TTAAGTTTTG	TAGAAAGGAA	TTTAATTGCT	240
CGTTCTCTAA	CAATGTCCTC	TCCTTGAAGT	ATTGGCTGA	ACAACCCACC	TNAAGTCCCT	300
TTGTGCATCC	ATTTTAAATA	TACTTAATAG	GGCATTGGTN	CACTAGGTTA	AATTCTGCAA	360
GAGTCATCTG	TCTGCAAAAG	TTGCGTTAGT	ATATCTGCCA			400

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 480 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

GAGCTCGGAT	CCAATAATCT	TTGTCTGAGG	GCAGCACACA	TATNCAGTGC	CATGGNAACT	60
GGTCTACCCC	ACATGGGAGC	AGCATGCCGT	AGNTATATAA	GGTCATTCCC	TGAGTCAGAC	120
ATGCCCTCTT	GACTACCGTG	TGCCAGTGCT	GGTGATTCTC	ACACACCTCC	NNCCGCTCTT	180
TGTGGAAAAA	CTGGCACTTG	NCTGGAACCT	GCAAGACATC	ACTTACAAAT	TCACCCACGA	240
GACACTTGAA	AGGTGTAACA	AAGCGACTCT	TGCATTGCTT	TTTGTCCCTC	CGGCACCAGT	300
TGTCAATACT	AACCCGCTGG	TTTGCCTCCA	TCACATTTGT	GATCTGTAGC	TCTGGATACA	360
TCTCCTGACA	GTACTGAAGA	ACTTCTTCTT	TTGTTTCAAA	AGCAACTCTT	GGTGCCTGTT	420
NGATCAGGTT	CCCATTTCCC	AGTCCGAATG	TTCACATGGC	ATATNTTACT	TCCCACAAAA	480

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 477 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

ATACAGCCCA	NATCCCACCA	CGAAGATGCG	CTTGTTGACT	GAGAACCTGA	TGCGGTCACT	60
GGTCCCCTG	TAGCCCCAGC	GA CTCTCCAC	CTGCTGGAAG	CGGTTGATGC	TGCACTCCTT	120
CCCACGCAGG	CAGCAGCGGG	GCCGGTCAAT	GA ACTCCACT	CGTGGCTTGG	GGTTGACGGT	180
TAANTGCAGG	AAGAGGCTGA	CCACCTCGCG	GTCCACCAGG	ATGCCC GACT	GTGCGGGACC	240
TGCAGCGAAA	CTCCTCGATG	GTCATGAGCG	GGAAGCGAAT	GANGCCCAGG	GCCTTGCCCA	300
GAACCTTCCG	CCTGTTCTCT	GGCGTCACCT	GCAGCTGCTG	CCGCTNACAC	TCGGCCTCGG	360
ACCAGCGGAC	AAACGGCGTT	GAACAGCCGC	ACCTCACGGA	TGCCCANTGT	GTCGCGCTCC	420
AGGAACGGCN	CCAGCGTGTC	CAGGTCAATG	TCGGTGAANC	CTCCGCGGGT	AATGGCG	477

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

GAACGGCTGG	ACCTTGCCTC	GCATTGTGCT	GCTGGCAGGA	ATACCTTGCC	AAGCAGCTCC	60
AGTCCGAGCA	GCCCCAGACC	GCTGCCGCCC	GAAGCTAAGC	CTGCCTCTGG	CCTTCCCCTC	120
CGCCTCAATG	CAGAACCANT	AGTGGGAGCA	CTGTGTTTAG	AGTTAAGAGT	GAACACTGTN	180
TGATTTTACT	TGGGAATTTT	CTCTGTTATA	TAGCTTTTCC	CAATGCTAAT	TTCCAAACAA	240
CAACAACAAA	ATAACATGTT	TGCCTGTTNA	GTTGTATAAA	AGTANGTGAT	TCTGTATNTA	300
AAGAAAATAT	TACTGTTACA	TATACTGCTT	GCAANTTCTG	TATTTATTGG	TNCTCTGGAA	360
ATAAATATAT	TATTAAA					377

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 495 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

CCCTTTGAGG	GGTTAGGGTC	CAGTTCCCAG	TGGAAGAAAC	AGGCCAGGAG	AANTGCGTGC	60
CGAGCTGANG	CAGATTTCCC	ACAGTGACCC	CAGAGCCCTG	GGCTATAGTC	TCTGACCCCT	120
CCAAGGAAAG	ACCACCTTCT	GGGGACATGG	GCTGGAGGGC	AGGACCTAGA	GGCACCAAGG	180
GAAGGCCCCA	TTCCGGGGCT	GTTCCCCGAG	GAGGAAGGGA	AGGGGCTCTG	TGTGCCCCCC	240
ACGAGGAANA	GGCCCTGANT	CCTGGGATCA	NACACCCCTT	CACGTGTATC	CCCACACAAA	300

TGCAAGCTCA	CCAAGGTCCC	CTCTCAGTCC	CTTCCCTACA	CCCTGAACGG	NCACTGGCCC	360
ACACCCACCC	AGANCANCCA	CCCGCCATGG	GGAATGTNCT	CAAGGAATCG	CNGGGCAACG	420
TGGACTCTNG	TCCCNNAAGG	GGGCAGAATC	TCCAATAGAN	GGANNGAACC	CTTGCTNANA	480
AAAAAAAAANA	AAAAA					495

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 472 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

GGTTACTTGG	TTTCATTGCC	ACCACTTAGT	GGATGTCATT	TAGAACCATT	TTGTCTGCTC	60
CCTCTGGAAG	CCTTGCGCAG	AGCGGACTTT	GTAATTGTTG	GAGAATAACT	GCTGAATTTT	120
TAGCTGTTTT	GAGTTGATTG	GCACCACTGC	ACCACAACCTC	AATATGAAAA	CTATTTNACT	180
TATTTATTAT	CTTGTAAGAA	GTATACAATG	AAAATTTTGT	TCATACTGTA	TTTATCAAGT	240
ATGATGAAAA	GCAATAGATA	TATATTCTTT	TATTATGTTN	AATTATGATT	GCCATTATTA	300
ATCGGCAAAA	TGTGGAGTGT	ATGTTCTTTT	CACAGTAATA	TATGCCTTT	GTAACCTCAC	360
TTGGTTATTT	TATTGTAAAT	GAATTACAAA	ATTCTTAATT	TAAGAAAATG	GTANGTTATA	420
TTTANTTCAN	TAATTCTTTT	CCTTGTTTAC	GTTAATTTTG	AAAAGAATGC	AT	472

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

CTGAAGCATT	TCTTCAAAC	TNTCTACTTT	TGTCATTGAT	ACCTGTAGTA	AGTTGACAAT	60
GTGGTGAAAT	TTCAAAATTA	TATGTAACTT	CTACTAGTTT	TACTTTCTCC	CCCAAGTCTT	120
TTTTAACTCA	TGATTTTTAC	ACACACAATC	CAGAACTTAT	TATATAGCCT	CTAAGTCTTT	180
ATTCTTCACA	GTAGATGATG	AAAGAGTCCT	CCAGTGTCTT	GNGCANAATG	TTCTAGNTAT	240
AGCTGGATAC	ATACNGTGGG	AGTTCTATAA	ACTCATACCT	CAGTGGGACT	NAACCAAAAT	300
TGTGTTAGTC	TCAATTCCTA	CCACACTGAG	GGAGCCTCCC	AAATCACTAT	ATTCTTATCT	360
GCAGGTACTC	CTCCAGAAAA	ACNGACAGGG	CAGGCTTGCA	TGAAAAAGTN	ACATCTGCGT	420
TACAAAGTCT	ATCTTCCTCA	NANGTCTGTN	AAGGAACAAT	TTAATCTTCT	AGCTTT	476

(2) INFORMATION FOR SEQ ID NO:97:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 479 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

ACTCTTTCTA	ATGCTGATAT	GATCTTGAGT	ATAAGAATGC	ATATGTCACT	AGAATGGATA	60
AAATAATGCT	GCAAACTTAA	TGTTCTTATG	CAAAATGGAA	CGCTAATGAA	ACACAGCTTA	120
CAATCGCAAA	TCAAACTCA	CAAGTGCTCA	TCTGTTGTAG	ATTTAGTGTA	ATAAGACTTA	180
GATTGTGCTC	CTTCGATAT	GATTGTTTCT	CANATCTTGG	GCAATNTTCC	TTAGTCAAAT	240
CAGGCTACTA	GAATTCTGTT	ATTGGATATN	TGAGAGCATG	AAATTTTAA	NAATACACTT	300
GTGATTATNA	AATTAATCAC	AAATTTCACT	TATACCTGCT	ATCAGCAGCT	AGAAAAACAT	360
NTNNTTTT	NATCAAAGTA	TTTTGTGTTT	GGAANTGTNN	AAATGAAATC	TGAATGTGGG	420
TTCNATCTTA	TTTTTCCCN	GACNACTANT	TNCTTTT	TGA	CCATC	479

(2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 461 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

AGTGACTTGT	CCTCCAACAA	AACCCCTTGA	TCAAGTTTGT	GGCACTGACA	ATCAGACCTA	60
TGCTAGTTCC	TGTCATCTAT	TCGCTACTAA	ATGCAGACTG	GAGGGGACCA	AAAAGGGGCA	120
TCAACTCCAG	CTGGATTATT	TTGGAGCCTG	CAAATCTATT	CCTACTTGTA	CGGACTTTGA	180
AGTGATTGAG	TTTCTCTAC	GGATGAGAGA	CTGGCTCAAG	AATATCCTCA	TGCAGCTTTA	240
TGAAGCCACT	CTGAACACGC	TGGTTATCTA	GATGAGAACA	GAGAAATAAA	GTCAGAAAAT	300
TTACCTGGAG	AAAAGAGGCT	TTGGCTGGGG	ACCATCCCAT	TGAACCTTCT	CTTAAGGACT	360
TTAAGAAAAA	CTACCACATG	TTGTGTATCC	TGGTGCCGGC	CGTTTATGAA	CTGACCACCC	420
TTTGGAATAA	TCTTGACGCT	CCTGAACTTG	CTCCTCTGCG	A		461

(2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 171 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

GTGGCCGCGC GCAGGTGTTT CCTCGTACCG CAGGGCCCCC TCCCTTCCCC AGGCGTCCCT	60
CGGCGCCTCT GCGGGCCCGA GGAGGAGCGG CTGGCGGGTG GGGGGAGTGT GACCCACCCT	120
CGGTGAGAAA AGCCTTCTCT AGCGATCTGA GAGGCGTGCC TTGGGGGTAC C	171

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

CGGCCGCAAG TGCAACTCCA GCTGGGGCCG TGCGGACGAA GATTCTGCCA GCAGTTGGTC	60
CGACTGCGAC GACGGCGGCG GCGACAGTCG CAGGTGCAGC GCGGGCGCCT GGGGTCTTGC	120
AAGGCTGAGC TGACGCCGCA GAGGTCGTGT CACGTCCCAC GACCTTGACG CCGTCGGGGA	180
CAGCCGGAAC AGAGCCCGGT GAAGCGGGAG GCCTCGGGGA GCCCTCGGG AAGGGCGGCC	240
CGAGAGATAC GCAGGTGCAG GTGGCCGCC	269

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

TTTTTTTTTT TTTTGAATC TACTGCGAGC ACAGCAGGTC AGCAACAAGT TTATTTTGCA	60
GCTAGCAAGG TAACAGGGTA GGGCATGGTT ACATGTCAG GTCAACTTCC TTTGTCGTGG	120
TTGATTGGTT TGTCTTTATG GGGGCGGGGT GGGGTAGGGG AAACGAAGCA AATAACATGG	180
AGTGGGTGCA CCCTCCCTGT AGAACCTGGT TACAAAGCTT GGGGCAGTTC ACCTGGTCTG	240
TGACCGTCAT TTTCTTGACA TCAATGTTAT TAGAAGTCAG GATATCTTTT AGAGAGTCCA	300
CTGTTCTGGA GGGAGATTAG GGTTCCTTGC CAAATCCAAC AAAATCCACT GAAAAAGTTG	360
GATGATCAGT ACGAATACCG AGGCATATTC TCATATCGGT GGCCA	405

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 470 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	60
GGCACTTAAT	CCATTTTAT	TCAAAATGT	CTACAAATTT	AATCCCATTA	TACGGTATTT	120
TCAAAATCTA	AATTATTCAA	ATTAGCCAAA	TCCTTACCAA	ATAATACCCA	AAAATCAAAA	180
ATATACTTCT	TTCAGCAAAC	TTGTTACATA	AATTAAAAAA	ATATATACGG	CTGGTGTTTT	240
CAAAGTACAA	TTATCTTAAC	ACTGCAAACA	TTTAAGGAA	CTAAAATAAA	AAAAAACACT	300
CCGCAAAGGT	TAAAGGGAAC	AACAAATTCT	TTTACAACAC	CATTATAAAA	ATCATATCTC	360
AAATCTTAGG	GGAATATATA	CTTCACACGG	GATCTTAACT	TTTACTCACT	TTGTTTATTT	420
TTTTAAACCA	TTGTTTGGGC	CCAACACAAT	GGAATCCCCC	CTGGACTAGT		470

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 581 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

TTTTTTTTTT	TTTTTTTTGA	CCCCCTCTT	ATAAAAACA	AGTTACCATT	TTATTTTACT	60
TACACATATT	TATTTTATAA	TTGGTATTAG	ATATTCAAAA	GGCAGCTTTT	AAAATCAAAC	120
TAAATGGAAA	CTGCCTTAGA	TACATAATTC	TTAGGAATTA	GCTTAAAATC	TGCCTAAAGT	180
GAAAATCTTC	TCTAGCTCTT	TTGACTGTAA	ATTTTGTACT	CTTGTAATAAC	ATCCAAATTC	240
ATTTTCTTG	TCTTTAAAAT	TATCTAATCT	TTCCATTTTT	TCCCTATTCC	AAGTCAATTT	300
GCTTCTCTAG	CCTCATTTCC	TAGCTCTTAT	CTACTATTAG	TAAGTGGCTT	TTTCCTAAA	360
AGGGAAAACA	GGAAGAGAAA	TGGCACACAA	AACAAACATT	TTATATTCAT	ATTCTACCT	420
ACGTTAATAA	AATAGCATTT	TGTGAAGCCA	GCTCAAAAGA	AGGCTTAGAT	CCTTTTATGT	480
CCATTTTAGT	CACTAAACGA	TATCAAAGTG	CCAGAATGCA	AAAGGTTTGT	GAACATTTAT	540
TCAAAAGCTA	ATATAAGATA	TTTCACATAC	TCATCTTTCT	G		581

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 578 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

TTTTTTTTTT	TTTTTTTTTT	TTTTTCTCTT	CTTTTTTTTT	GAAATGAGGA	TCGAGTTTTT	60
CACTCTCTAG	ATAGGGCATG	AAGAAACTC	ATCTTTCCAG	CTTTAAAATA	ACAATCAAAT	120
CTCTTATGCT	ATATCATATT	TTAAGTTAAA	CTAATGAGTC	ACTGGCTTAT	CTTCTCCTGA	180
AGGAAATCTG	TTCATTCCTT	TCATTCATAT	AGTTATATCA	AGTACTACCT	TGCATATTGA	240
GAGGTTTTTC	TTCTCTATTT	ACACATATAT	TTCCATGTGA	ATTTGTATCA	AACCTTTATT	300
TTCATGCAAA	CTAGAAAATA	ATGTTTCTTT	TGCATAAGAG	AAGAGAACAA	TATAGCATT	360
CAAACTGCT	CAAATTGTTT	GTTAAGTTAT	CCATTATAAT	TAGTTGGCAG	GAGCTAATAC	420
AAATCACATT	TACGACAGCA	ATAATAAAAC	TGAAGTACCA	GTAAATATC	CAAATAATT	480
AAAGGAACAT	TTTAGCCTG	GGTATAATTA	GCTAATTCAC	TTTACAAGCA	TTTATTAGAA	540
TGAATTCACA	TGTTATTATT	CCTAGCCCAA	CACAATGG			578

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 538 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

TTTTTTTTTT	TTTTTCAGTA	ATAATCAGAA	CAATATTTAT	TTTTATATTT	AAAATTCATA	60
GAAAAGTGCC	TTACATTTAA	TAAAAGTTTG	TTTCTCAAAG	TGATCAGAGG	AATTAGATAT	120
GTCTTGAACA	CCAATATTAA	TTTGAGGAAA	ATACACCAAA	ATACATTAAAG	TAAATTATTT	180
AAGATCATAG	AGCTTGTAAG	TGAAAAGATA	AAATTTGACC	TCAGAAACTC	TGAGCATTAA	240
AAATCCACTA	TTAGCAAATA	AATTACTATG	GACTTCTTGC	TTTAATTTTG	TGATGAATAT	300
GGGTGTGCAC	TGGTAAACCA	ACACATTCTG	AAGGATACAT	TACTTAGTGA	TAGATTCTTA	360
TGTACTTTGC	TAATACGTGG	ATATGAGTTG	ACAAGTTTCT	CTTCTTCAA	TCTTTTAAAG	420
GGCGAGAAAT	GAGGAAGAAA	AGAAAAGGAT	TACGCATACT	GTTCTTTCTA	TGGAAGGATT	480
AGATATGTTT	CCTTTGCCAA	TATTAATAAA	ATAATAATGT	TTACTACTAG	TGAAACCC	538

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 473 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

TTTTTTTTTT	TTTTTTAGTC	AAGTTTCTAT	TTTTATTATA	ATTAAAGTCT	TGGTCATTTC	60
ATTTATTAGC	TCTGCAACTT	ACATATTTAA	ATTAAAGAAA	CGTTTTAGAC	AACTGTACAA	120
TTTATAAATG	TAAGGTGCCA	TTATTGAGTA	ATATATTCCCT	CCAAGAGTGG	ATGTGTCCCT	180
TCTCCCACCA	ACTAATGAAC	AGCAACATTA	GTTTAATTTT	ATTAGTAGAT	ATACACTGCT	240
GCAAACGCTA	ATTCTCTTCT	CCATCCCCAT	GTGATATTGT	GTATATGTGT	GAGTTGGTAG	300
AATGCATCAC	AATCTACAAT	CAACAGCAAG	ATGAAGCTAG	GCTGGGCTTT	CGGTGAAAAAT	360
AGACTGTGTC	TGTCTGAATC	AAATGATCTG	ACCTATCCTC	GGTGGCAAGA	ACTCTTCGAA	420
CCGCTTCCTC	AAAGGCGCTG	CCACATTGTG	GGCTCTTTGC	ACTTGTTTCA	AAA	473

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1621 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

CGCCATGGCA	CTGCAGGGCA	TCTCGGTCAT	GGAGCTGTCC	GGCCTGGCCC	CGGGCCCGTT	60
CTGTGCTATG	GTCCCTGGCTG	ACTTCGGGGC	GCGTGTGGTA	CGCGTGGACC	GGCCCGGCTC	120
CCGCTACGAC	GTGAGCCGCT	TGGGCCGGGG	CAAGCGCTCG	CTAGTGCTGG	ACCTGAAGCA	180
GCCGCGGGGA	GCCGCCGTGC	TGCGGCGTCT	GTGCAAGCGG	TCGGATGTGC	TGCTGGAGCC	240
CTTCCGCCGC	GGTGTCTATG	AGAAACTCCA	GCTGGGCCCC	GAGATTCTGC	AGCGGGAAAA	300
TCCAAGGCTT	ATTTATGCCA	GGCTGAGTGG	ATTGCGCCAG	TCAGGAAGCT	TCTGCCGGTT	360
AGCTGGCCAC	GATATCAACT	ATTGGCTTTT	GTCAGGTGTT	CTCTCAAAAA	TTGGCAGAAG	420
TGGTGAGAAT	CCGTATGCCC	CGCTGAATCT	CCTGGCTGAC	TTTGCTGGTG	GTGGCCTTAT	480
GTGTGCACTG	GGCATTATAA	TGGCTCTTTT	TGACCGCACA	CGCACTGACA	AGGGTCAGGT	540
CATTGATGCA	AATATGGTGG	AAGGAACAGC	ATATTTAAGT	TCTTTTCTGT	GGAAAACTCA	600
GAAATCGAGT	CTGTGGGAAG	CACCTCGAGG	ACAGAACATG	TTGGATGGTG	GAGCACCTTT	660
CTATACGACT	TACAGGACAG	CAGATGGGGA	ATTCATGGCT	GTTGGAGCAA	TAGAACCCCA	720
GTTCTACGAG	CTGCTGATCA	AAGGACTTGG	ACTAAAGTCT	GATGAACTTC	CCAATCAGAT	780
GAGCATGGAT	GATTGGCCAG	AAATGAAGAA	GAAGTTTGCA	GATGTATTTG	CAAAGAAGAC	840
GAAGGCAGAG	TGGTGTCAAA	TCTTTGACGG	CACAGATGCC	TGTGTGACTC	CGGTTCTGAC	900
TTTTGAGGAG	GTTGTTTCATC	ATGATCACAA	CAAGGAACGG	GGCTCGTTTA	TCACCAGTGA	960
GGAGCAGGAC	GTGAGCCCCC	GCCCTGCACC	TCTGCTGTTA	AACACCCAG	CCATCCCTTC	1020
TTTCAAAAGG	GATCCTTTCA	TAGGAGAACA	CACTGAGGAG	ATACTTGAAG	AATTTGGATT	1080
CAGCCGCGAA	GAGATTTATC	AGCTTAACTC	AGATAAAATC	ATTGAAAGTA	ATAAGGTAAA	1140
AGCTAGTCTC	TAACTTCCAG	GCCCACGGCT	CAAGTGAATT	TGAATACTGC	ATTACAGTG	1200
TAGAGTAACA	CATAACATTG	TATGCATGGA	AACATGGAGG	AACAGTATTA	CAGTGTCCCTA	1260
CCACTCTAAT	CAAGAAAAGA	ATTACAGACT	CTGATTCTAC	AGTGATGATT	GAATTCTAAA	1320
AATGGTTATC	ATTAGGGCTT	TTGATTTATA	AAACTTTGGG	TACTTATACT	AAATTATGGT	1380
AGTTATTCTG	CCTTCCAGTT	TGCTTGATAT	ATTTGTTGAT	ATTAAGATTC	TTGACTTATA	1440
TTTTGAATGG	GTTCTAGTGA	AAAAGGAATG	ATATATTCTT	GAAGACATCG	ATATACATTT	1500
ATTTACACTC	TTGATTCTAC	AATGTAGAAA	ATGAGGAAAT	GCCACAAATT	GTATGGTGAT	1560

AAAAGTCACG TGAAACAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1620
A 1621

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 382 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

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Met Ala Leu Gln Gly Ile Ser Val Met Glu Leu Ser Gly Leu Ala Pro
1           5           10           15
Gly Pro Phe Cys Ala Met Val Leu Ala Asp Phe Gly Ala Arg Val Val
20           25           30
Arg Val Asp Arg Pro Gly Ser Arg Tyr Asp Val Ser Arg Leu Gly Arg
35           40           45
Gly Lys Arg Ser Leu Val Leu Asp Leu Lys Gln Pro Arg Gly Ala Ala
50           55           60
Val Leu Arg Arg Leu Cys Lys Arg Ser Asp Val Leu Leu Glu Pro Phe
65           70           75           80
Arg Arg Gly Val Met Glu Lys Leu Gln Leu Gly Pro Glu Ile Leu Gln
85           90           95
Arg Glu Asn Pro Arg Leu Ile Tyr Ala Arg Leu Ser Gly Phe Gly Gln
100          105          110
Ser Gly Ser Phe Cys Arg Leu Ala Gly His Asp Ile Asn Tyr Leu Ala
115          120          125
Leu Ser Gly Val Leu Ser Lys Ile Gly Arg Ser Gly Glu Asn Pro Tyr
130          135          140
Ala Pro Leu Asn Leu Leu Ala Asp Phe Ala Gly Gly Gly Leu Met Cys
145          150          155          160
Ala Leu Gly Ile Ile Met Ala Leu Phe Asp Arg Thr Arg Thr Asp Lys
165          170          175
Gly Gln Val Ile Asp Ala Asn Met Val Glu Gly Thr Ala Tyr Leu Ser
180          185          190
Ser Phe Leu Trp Lys Thr Gln Lys Ser Ser Leu Trp Glu Ala Pro Arg
195          200          205
Gly Gln Asn Met Leu Asp Gly Gly Ala Pro Phe Tyr Thr Thr Tyr Arg
210          215          220
Thr Ala Asp Gly Glu Phe Met Ala Val Gly Ala Ile Glu Pro Gln Phe
225          230          235          240
Tyr Glu Leu Leu Ile Lys Gly Leu Gly Leu Lys Ser Asp Glu Leu Pro
245          250          255
Asn Gln Met Ser Met Asp Asp Trp Pro Glu Met Lys Lys Lys Phe Ala
260          265          270
Asp Val Phe Ala Lys Lys Thr Lys Ala Glu Trp Cys Gln Ile Phe Asp
275          280          285
Gly Thr Asp Ala Cys Val Thr Pro Val Leu Thr Phe Glu Glu Val Val

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290	295	300
His His Asp His Asn Lys Glu Arg Gly Ser Phe Ile Thr Ser Glu Glu		
305	310	315
Gln Asp Val Ser Pro Arg Pro Ala Pro Leu Leu Leu Asn Thr Pro Ala		320
	325	330
Ile Pro Ser Phe Lys Arg Asp Pro Phe Ile Gly Glu His Thr Glu Glu		335
	340	345
Ile Leu Glu Glu Phe Gly Phe Ser Arg Glu Glu Ile Tyr Gln Leu Asn		350
	355	360
Ser Asp Lys Ile Ile Glu Ser Asn Lys Val Lys Ala Ser Leu		365
370	375	380

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1524 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

GGCACGAGGC	TGCGCCAGGG	CCTGAGCGGA	GGCGGGGGCA	GCCTCGCCAG	CGGGGGCCCC	60
GGGCCTGGCC	ATGCCTCACT	GAGCCAGCGC	CTGCGCCTCT	ACCTCGCCGA	CAGCTGGAAC	120
CAGTGCGACC	TAGTGGCTCT	CACCTGCTTC	CTCCTGGGCG	TGGGCTGCCG	GCTGACCCCG	180
GGTTTGTACC	ACCTGGGCCG	CACTGTCCTC	TGCATCGACT	TCATGGTTTT	CACGGTGCGG	240
CTGCTTCACA	TCTTCACGGT	CAACAAACAG	CTGGGGCCCC	AGATCGTCAT	CGTGAGCAAG	300
ATGATGAAGG	ACGTGTTCTT	CTTCCTCTTC	TTCTCTGGCG	TGTGGCTGGT	AGCCTATGGC	360
GTGGCCACGG	AGGGGCTCCT	GAGGCCACGG	GACAGTGACT	TCCCAAGTAT	CCTGCGCCGC	420
GTCTTCTACC	GTCCCTACCT	GCAGATCTTC	GGGCAGATTG	CCCAGGAGGA	CATGGACGTG	480
GCCCTCATGG	AGCACAGCAA	CTGCTCGTCG	GAGCCCGGCT	TCTGGGCACA	CCCTCCTGGG	540
GGCCAGGCGG	GCACCTGCGT	CTCCCAGTAT	GCCAACTGGC	TGGTGGTGCT	GCTCCTCGTC	600
ATCTTCCTGC	TCGTGGCCAA	CATCCTGCTG	GTCAACTTGC	TCATTGCCAT	GTTCAGTTAC	660
ACATTTCGCA	AAGTACAGGG	CAACAGCGAT	CTCTACTGGA	AGGCGCAGCG	TTACCGCCTC	720
ATCCGGGAAT	TCCACTCTCG	GCCCGCGCTG	GCCCCGCCCT	TTATCGTCAT	CTCCCACTTG	780
CGCCTCCTGC	TCAGGCAATT	GTGCAGGCGA	CCCCGGAGCC	CCCAGCCGTC	CTCCCCGGCC	840
CTCGAGCATT	TCCGGGTTTA	CCTTTCTAAG	GAAGCCGAGC	GGAAGCTGCT	AACGTGGGAA	900
TCGGTGCATA	AGGAGAACTT	TCTGCTGGCA	CGCGCTAGGG	ACAAGCGGGA	GAGCGACTCC	960
GAGCGTCTGA	AGCGCACGTC	CCAGAAGGTG	GACTTGGCAC	TGAAACAGCT	GGGACACATC	1020
CGCGAGTACG	AACAGCGCCT	GAAAGTGCTG	GAGCGGGAGG	TCCAGCAGTG	TAGCCGCGTC	1080
CTGGGGTGCG	TGGCCGAGGC	CCTGAGCCGC	TCTGCCCTTG	TGCCCCCAGG	TGGGCCGCCA	1140
CCCCCTGACC	TGCCTGGGTC	CAAAGACTGA	GCCCTGCTGG	CGGACTTCAA	GGAGAAGCCC	1200
CCACAGGGGA	TTTGTCTCCT	AGAGTAAGGC	TCATCTGGGC	CTCGGCCCCC	GCACCTGGTG	1260
GCCTTGCTCT	TGAGGTGAGC	CCCATGTCCA	TCTGGGCCAC	TGTCAGGACC	ACCTTTGGGA	1320
GTGTATCCTT	TACAAACCAC	AGCATGCCCG	GCTCCTCCCA	GAACCAGTCC	CAGCCTGGGA	1380
GGATCAAGGC	CTGGATCCCG	GGCCGTTATC	CATCTGGAGG	CTGCAGGGTC	CTTGGGGTAA	1440
CAGGGACCAC	AGACCCCTCA	CCACTCACAG	ATTCCTCACA	CTGGGGAAAT	AAAGCCATTT	1500
CAGAGGAAAA	AAAAAAAAAA	AAAA				1524

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3410 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

GGGAACCAGC	CTGCACGCGC	TGGCTCCGGG	TGACAGCCGC	GCGCCTCGGC	CAGGATCTGA	60
GTGATGAGAC	GTGTCCCCAC	TGAGGTGCCC	CACAGCAGCA	GGTGTGAGC	ATGGGCTGAG	120
AAGCTGGACC	GGCACCAAAG	GGCTGGCAGA	AATGGGCGCC	TGGCTGATTC	CTAGGCAGTT	180
GGCGGCAGCA	AGGAGGAGAG	GCCGCAGCTT	CTGGAGCAGA	GCCGAGACGA	AGCAGTTCTG	240
GAGTGCCTGA	ACGGCCCCCT	GAGCCCTACC	CGCCTGGCCC	ACTATGGTCC	AGAGGCTGTG	300
GGTGAGCCGC	CTGCTGCGGC	ACCGGAAAGC	CCAGCTCTTG	CTGGTCAACC	TGCTAACCTT	360
TGGCCTGGAG	GTGTGTTTGG	CCGCAGGCAT	CACCTATGTG	CCGCTCTGCG	TGCTGGAAGT	420
GGGGGTAGAG	GAGAAGTTCA	TGACCATGGT	GCTGGGCATT	GGTCCAGTGC	TGGGCCTGGT	480
CTGTGTCCCG	CTCCTAGGCT	CAGCCAGTGA	CCACTGGCGT	GGACGCTATG	GCCGCCGCCG	540
GCCCTTCATC	TGGGCACTGT	CCTTGGGCAT	CCTGCTGAGC	CTCTTTCTCA	TCCCAAGGGC	600
CGGCTGGCTA	GCAGGGCTGC	TGTGCCCCGA	TCCAGGCCCC	CTGGAGCTGG	CACTGCTCAT	660
CCTGGGCGTG	GGGCTGCTGG	ACTTCTGTGG	CCAGGTGTGC	TTCACTCCAC	TGGAGGCCCT	720
GCTCTCTGAC	CTCTTCCGGG	ACCCGGACCA	CTGTCGCCAG	GCCTACTCTG	TCTATGCCTT	780
CATGATCAGT	CTTGGGGGCT	GCCTGGGCTA	CCTCCTGCCT	GCCATTGACT	GGGACACCAG	840
TGCCCTGGCC	CCCTACCTGG	GCACCCAGGA	GGAGTGCCTC	TTTGGCCTGC	TCACCCTCAT	900
CTTCCTCACC	TGCGTAGCAG	CCACACTGCT	GGTGGCTGAG	GAGGCAGCGC	TGGGCCCCAC	960
CGAGCCAGCA	GAAGGGCTGT	CGGCCCCCTC	CTTGTCGCCC	CACTGCTGTC	CATGCCGGGC	1020
CCGCTTGGCT	TTCCGGAACC	TGGGCGCCCT	GCTTCCCCGG	CTGCACCAGC	TGTGTGCCCG	1080
CATGCCCCGC	ACCCTGCGCC	GGCTCTTCGT	GGCTGAGCTG	TGCAGCTGGA	TGGCACTCAT	1140
GACCTTCACG	CTGTTTTACA	CGGATTTTCG	GGGCGAGGGG	CTGTACCAGG	GCGTGCCAG	1200
AGCTGAGCCG	GGCACCGAGG	CCCGGAGACA	CTATGATGAA	GGCGTTCGGA	TGGGCAGCCT	1260
GGGGCTGTTC	CTGCAGTGCG	CCATCTCCCT	GGTCTTCTCT	CTGGTCATGG	ACCGGCTGGT	1320
GCAGCGATTG	GGCACTCGAG	CAGTCTATTT	GGCCAGTGTG	GCAGCTTTCC	CTGTGCTGTC	1380
CGGTGCCACA	TGCCTGTCCC	ACAGTGTGGC	CGTGGTGACA	GCTTCAGCCG	CCCTCACCGG	1440
GTTACCTTC	TCAGCCCTGC	AGATCCTGCC	CTACACACTG	GCCTCCCTCT	ACCACCGGGA	1500
GAAGCAGGTG	TCCTGCCCCA	AATACCGAGG	GGACACTGGA	GGTGCTAGCA	GTGAGGACAG	1560
CCTGATGACC	AGCTTCCTGC	CAGGCCCTAA	GCCTGGAGCT	CCCTTCCCTA	ATGGACACGT	1620
GGGTGCTGGA	GGCAGTGGCC	TGCTCCCACC	TCCACCCGCG	CTCTGCGGGG	CCTCTGCCTG	1680
TGATGTCTCC	GTACGTGTGG	TGGTGGGTGA	GCCCACCGAG	GCCAGGGTGG	TTCCGGGCCG	1740
GGGCATCTGC	CTGGACCTCG	CCATCCTGGA	TAGTGCCTTC	CTGCTGTCCC	AGGTGGCCCC	1800
ATCCCTGTTT	ATGGGCTCCA	TTGTCCAGCT	CAGCCAGTCT	GTCAGTGCCT	ATATGGTGTC	1860
TGCCGAGGCG	CTGGGTCTGG	TCGCCATTTA	CTTTGCTACA	CAGGTAGTAT	TTGACAAGAG	1920
CGACTTGGCC	AAATACTCAG	CGTAGAAAAC	TTCCAGCACA	TTGGGGTGGG	GGGCCTGCCT	1980
CACTGGGTCC	CAGCTCCCCG	CTCCTGTTAG	CCCCATGGGG	CTGCCGGGCT	GGCCGCCAGT	2040
TTCTGTTGCT	GCCAAAGTAA	TGTGGCTCTC	TGCTGCCACC	CTGTGCTGCT	GAGGTGCGTA	2100
GCTGCACAGC	TGGGGGCTGG	GGCGTCCCTC	TCCTCTCTCC	CCAGTCTCTA	GGGCTGCCTG	2160
ACTGGAGGCC	TTCCAAGGGG	GTTTCAGTCT	GGACTTATAC	AGGGAGGCCA	GAAGGGCTCC	2220
ATGCACTGGA	ATGCGGGGAC	TCTGCAGGTG	GATTACCCAG	GCTCAGGGTT	AACAGCTAGC	2280
CTCCTAGTTG	AGACACACCT	AGAGAAGGGT	TTTTGGGAGC	TGAATAAACT	CAGTCACCTG	2340
GTTTCCCATC	TCTAAGCCCC	TTAACCTGCA	GCTTCGTTTA	ATGTAGCTCT	TGCATGGGAG	2400
TTTCTAGGAT	GAAACACTCC	TCCATGGGAT	TTGAACATAT	GACTTATTTG	TAGGGGAAGA	2460

GTCTTGAGGG	GCAACACACA	AGAACCAGGT	CCCCTCAGCC	CACAGCACTG	TCTTTTTGCT	2520
GATCCACCCC	CCTCTTACCT	TTTATCAGGA	TGTGGCCTGT	TGGTCCTTCT	GTTGCCATCA	2580
CAGAGACACA	GGCATTAAAA	TATTTAACTT	ATTTATTTAA	CAAAGTAGAA	GGGAATCCAT	2640
TGCTAGCTTT	TCTGTGTTGG	TGTCTAATAT	TTGGGTAGGG	TGGGGGATCC	CCAACAATCA	2700
GGTCCCCCTGA	GATAGCTGGT	CATTGGGCTG	ATCATTGCCA	GAATCTTCTT	CTCCTGGGGT	2760
CTGGCCCCCCC	AAAATGCCTA	ACCCAGGACC	TTGGAAATTC	TACTCATCCC	AAATGATAAT	2820
TCCAAATGCT	GTTACCCAAG	GTTAGGGTGT	TGAAGGAAGG	TAGAGGGTGG	GGCTTCAGGT	2880
CTCAACGGCT	TCCCTAACCA	CCCCTCTTCT	CTTGGCCCAG	CCTGGTTCCC	CCCACTTCCA	2940
CTCCCCCTCTA	CTCTCTCTAG	GACTGGGCTG	ATGAAGGCAC	TGCCCCAAAT	TCCCCCTACC	3000
CCCAACTTTC	CCCTACCCCC	AACTTTCCCC	ACCAGCTCCA	CAACCCTGTT	TGGAGCTACT	3060
GCAGGACCAG	AAGCACAAAG	TGCGGTTTCC	CAAGCCTTTG	TCCATCTCAG	CCCCCAGAGT	3120
ATATCTGTGC	TTGGGGAATC	TCACACAGAA	ACTCAGGAGC	ACCCCTTGCC	TGAGCTAAGG	3180
GAGGCTTTAT	CTCTCAGGGG	GGGTTTAAAGT	GCCGTTTGCA	ATAATGTCGT	CTTATTTATT	3240
TAGCGGGGTG	AATATTTTAT	ACTGTAAGTG	AGCAATCAGA	GTATAATGTT	TATGGTGACA	3300
AAATTAAAGG	CTTTCTTATA	TGTTTAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	3360
AAAAAAAAARA	AAAAAAAAAA	AAAAAAAAAA	AAAAAATAA	AAAAAAAAAA		3410

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1289 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

AGCCAGGCGT	CCCTCTGCCT	GCCCACTCAG	TGGCAACACC	CGGGAGCTGT	TTTGTCTTTT	60
GTGGAGCCTC	AGCAGTTCCC	TCTTTCAGAA	CTCACTGCCA	AGAGCCCTGA	ACAGGAGCCA	120
CCATGACATG	CTTCAGCTTC	ATTAAGACCA	TGATGATCCT	CTTCAATTTG	CTCATCTTTC	180
TGTGTGGTGC	AGCCCTGTTG	GCAGTGGGCA	TCTGGGTGTC	AATCGATGGG	GCATCCTTTC	240
TGAAGATCTT	CGGGCCACTG	TCGTCCAGTG	CCATGCAGTT	TGTCAACGTG	GGCTACTTCC	300
TCATCGCAGC	CGGCGTTGTG	GTCTTTGCTC	TTGGTTTCCT	GGGCTGCTAT	GGTGCTAAGA	360
CTGAGAGCAA	GTGTGCCCTC	GTGACGTTCT	TCTTCATCCT	CCTCCTCATC	TTCATTGCTG	420
AGGTTGCAGC	TGCTGTGGTC	GCCTTGGTGT	ACACCACAAT	GGCTGAGCAC	TTCCTGACGT	480
TGCTGGTAGT	GCCTGCCATC	AAGAAAGATT	ATGGTTCCCA	GGAAGACTTC	ACTCAAGTGT	540
GGAACACCAC	CATGAAAGGG	CTCAAGTGCT	GTGGCTTCAC	CAACTATACG	GATTTTGAGG	600
ACTCACCTTA	CTTCAAAGAG	AACAGTGCCT	TTCCCCCATT	CTGTTGCAAT	GACAACGTCA	660
CCAACACAGC	CAATGAAACC	TGCACCAAGC	AAAAGGCTCA	CGACCAAAAA	GTAGAGGGTT	720
GCTTCAATCA	GCTTTTGTAT	GACATCCGAA	CTAATGCAGT	CACCGTGGGT	GGTGTGGCAG	780
CTGGAATTGG	GGGCCTCGAG	CTGGCTGCCA	TGATTGTGTC	CATGTATCTG	TACTGCAATC	840
TACAATAAGT	CCACTTCTGC	CTCTGCCACT	ACTGCTGCCA	CATGGGAATC	GTGAAGAGGC	900
ACCCTGGCAA	GCAGCAGTGA	TTGGGGGAGG	GGACAGGATC	TAACAATGTC	ACTTGGGCCA	960
GAATGGACCT	GCCCTTTCTG	CTCCAGACTT	GGGGCTAGAT	AGGGACCACT	CCTTTTAGCG	1020
ATGCCTGACT	TTCCTTCCAT	TGGTGGGTGG	ATGGGTGGGG	GGCATTCCAG	AGCCTCTAAG	1080
GTAGCCAGTT	CTGTTGCCCA	TTCCCCAGT	CTATTAAACC	CTTGATATGC	CCCCTAGGCC	1140
TAGTGGTGAT	CCCAGTGCTC	TACTGGGGGA	TGAGAGAAAG	GCATTTTATA	GCCTGGGCAT	1200
AAGTGAAATC	AGCAGAGCCT	CTGGGTGGAT	GTGTAGAAGG	CACTTCAAAA	TGCATAAACC	1260
TGTTACAATG	TTAAAAAAA	AAAAAAA				1289

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

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Met Val Phe Thr Val Arg Leu Leu His Ile Phe Thr Val Asn Lys Gln
 1             5             10             15

Leu Gly Pro Lys Ile Val Ile Val Ser Lys Met Met Lys Asp Val Phe
      20             25             30

Phe Phe Leu Phe Phe Leu Gly Val Trp Leu Val Ala Tyr Gly Val Ala
 35             40             45

Thr Glu Gly Leu Leu Arg Pro Arg Asp Ser Asp Phe Pro Ser Ile Leu
 50             55             60

Arg Arg Val Phe Tyr Arg Pro Tyr Leu Gln Ile Phe Gly Gln Ile Pro
 65             70             75             80

Gln Glu Asp Met Asp Val Ala Leu Met Glu His Ser Asn Cys Ser Ser
      85             90             95

Glu Pro Gly Phe Trp Ala His Pro Pro Gly Ala Gln Ala Gly Thr Cys
      100             105             110

Val Ser Gln Tyr Ala Asn Trp Leu Val Val Leu Leu Leu Val Ile Phe
      115             120             125

Leu Leu Val Ala Asn Ile Leu Leu Val Asn Leu Leu Ile Ala Met Phe
      130             135             140

Ser Tyr Thr Phe Gly Lys Val Gln Gly Asn Ser Asp Leu Tyr Trp Lys
      145             150             155             160

Ala Gln Arg Tyr Arg Leu Ile Arg Glu Phe His Ser Arg Pro Ala Leu
      165             170             175

Ala Pro Pro Phe Ile Val Ile Ser His Leu Arg Leu Leu Leu Arg Gln
      180             185             190

Leu Cys Arg Arg Pro Arg Ser Pro Gln Pro Ser Ser Pro Ala Leu Glu
      195             200             205

His Phe Arg Val Tyr Leu Ser Lys Glu Ala Glu Arg Lys Leu Leu Thr

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210	215	220
Trp Glu Ser Val His Lys Glu Asn Phe Leu Leu Ala Arg Ala Arg Asp		
225	230	235 240
Lys Arg Glu Ser Asp Ser Glu Arg Leu Lys Arg Thr Ser Gln Lys Val		
	245	250 255
Asp Leu Ala Leu Lys Gln Leu Gly His Ile Arg Glu Tyr Glu Gln Arg		
	260	265 270
Leu Lys Val Leu Glu Arg Glu Val Gln Gln Cys Ser Arg Val Leu Gly		
	275	280 285
Trp Val Ala Glu Ala Leu Ser Arg Ser Ala Leu Leu Pro Pro Gly Gly		
	290	295 300
Pro Pro Pro Pro Asp Leu Pro Gly Ser Lys Asp		
305	310	315

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 553 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

Met Val Gln Arg Leu Trp Val Ser Arg Leu Leu Arg His Arg Lys Ala		
1	5	10 15
Gln Leu Leu Leu Val Asn Leu Leu Thr Phe Gly Leu Glu Val Cys Leu		
	20	25 30
Ala Ala Gly Ile Thr Tyr Val Pro Leu Leu Leu Glu Val Gly Val		
	35	40 45
Glu Glu Lys Phe Met Thr Met Val Leu Gly Ile Gly Pro Val Leu Gly		
	50	55 60
Leu Val Cys Val Pro Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly		
65	70	75 80
Arg Tyr Gly Arg Arg Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile		
	85	90 95
Leu Leu Ser Leu Phe Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu		
	100	105 110

Leu Cys Pro Asp Pro Arg Pro Leu Glu Leu Ala Leu Leu Ile Leu Gly
 115 120 125
 Val Gly Leu Leu Asp Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu
 130 135 140
 Ala Leu Leu Ser Asp Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala
 145 150 155 160
 Tyr Ser Val Tyr Ala Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr
 165 170 175
 Leu Leu Pro Ala Ile Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu
 180 185 190
 Gly Thr Gln Glu Glu Cys Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu
 195 200 205
 Thr Cys Val Ala Ala Thr Leu Leu Val Ala Glu Glu Ala Ala Leu Gly
 210 215 220
 Pro Thr Glu Pro Ala Glu Gly Leu Ser Ala Pro Ser Leu Ser Pro His
 225 230 235 240
 Cys Cys Pro Cys Arg Ala Arg Leu Ala Phe Arg Asn Leu Gly Ala Leu
 245 250 255
 Leu Pro Arg Leu His Gln Leu Cys Cys Arg Met Pro Arg Thr Leu Arg
 260 265 270
 Arg Leu Phe Val Ala Glu Leu Cys Ser Trp Met Ala Leu Met Thr Phe
 275 280 285
 Thr Leu Phe Tyr Thr Asp Phe Val Gly Glu Gly Leu Tyr Gln Gly Val
 290 295 300
 Pro Arg Ala Glu Pro Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly
 305 310 315 320
 Val Arg Met Gly Ser Leu Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu
 325 330 335
 Val Phe Ser Leu Val Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg
 340 345 350
 Ala Val Tyr Leu Ala Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala
 355 360 365
 Thr Cys Leu Ser His Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu
 370 375 380
 Thr Gly Phe Thr Phe Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala
 385 390 395 400

Ser	Leu	Tyr	His	Arg	Glu	Lys	Gln	Val	Phe	Leu	Pro	Lys	Tyr	Arg	Gly				
				405								410				415			
Asp	Thr	Gly	Gly	Ala	Ser	Ser	Glu	Asp	Ser	Leu	Met	Thr	Ser	Phe	Leu				
				420				425								430			
Pro	Gly	Pro	Lys	Pro	Gly	Ala	Pro	Phe	Pro	Asn	Gly	His	Val	Gly	Ala				
				435				440								445			
Gly	Gly	Ser	Gly	Leu	Leu	Pro	Pro	Pro	Pro	Ala	Leu	Cys	Gly	Ala	Ser				
				450				455								460			
Ala	Cys	Asp	Val	Ser	Val	Arg	Val	Val	Val	Gly	Glu	Pro	Thr	Glu	Ala				
465								470								475		480	
Arg	Val	Val	Pro	Gly	Arg	Gly	Ile	Cys	Leu	Asp	Leu	Ala	Ile	Leu	Asp				
				485								490						495	
Ser	Ala	Phe	Leu	Leu	Ser	Gln	Val	Ala	Pro	Ser	Leu	Phe	Met	Gly	Ser				
				500				505								510			
Ile	Val	Gln	Leu	Ser	Gln	Ser	Val	Thr	Ala	Tyr	Met	Val	Ser	Ala	Ala				
				515				520								525			
Gly	Leu	Gly	Leu	Val	Ala	Ile	Tyr	Phe	Ala	Thr	Gln	Val	Val	Phe	Asp				
				530				535								540			
Lys	Ser	Asp	Leu	Ala	Lys	Tyr	Ser	Ala											
545								550											

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Met Gln Cys Phe Ser Phe Ile Lys Thr Met Met Ile Leu Phe Asn Leu
1 5 10 15

Leu Ile Phe Leu Cys Gly Ala Ala Leu Leu Ala Val Gly Ile Trp Val
20 25 30

Ser Ile Asp Gly Ala Ser Phe Leu Lys Ile Phe Gly Pro Leu Ser Ser
35 40 45

Ser Ala Met Gln Phe Val Asn Val Gly Tyr Phe Leu Ile Ala Ala Gly

90

50		55		60
Val Val Val Phe Ala Leu Gly Phe Leu Gly Cys Tyr Gly Ala Lys Thr				
65		70		75
				80
Glu Ser Lys Cys Ala Leu Val Thr Phe Phe Phe Ile Leu Leu Leu Ile				
	85		90	95
Phe Ile Ala Glu Val Ala Ala Ala Val Val Ala Leu Val Tyr Thr Thr				
	100		105	110
Met Ala Glu His Phe Leu Thr Leu Leu Val Val Pro Ala Ile Lys Lys				
	115		120	125
Asp Tyr Gly Ser Gln Glu Asp Phe Thr Gln Val Trp Asn Thr Thr Met				
	130		135	140
Lys Gly Leu Lys Cys Cys Gly Phe Thr Asn Tyr Thr Asp Phe Glu Asp				
	145		150	155
				160
Ser Pro Tyr Phe Lys Glu Asn Ser Ala Phe Pro Pro Phe Cys Cys Asn				
	165		170	175
Asp Asn Val Thr Asn Thr Ala Asn Glu Thr Cys Thr Lys Gln Lys Ala				
	180		185	190
His Asp Gln Lys Val Glu Gly Cys Phe Asn Gln Leu Leu Tyr Asp Ile				
	195		200	205
Arg Thr Asn Ala Val Thr Val Gly Gly Val Ala Ala Gly Ile Gly Gly				
	210		215	220
Leu Glu Leu Ala Ala Met Ile Val Ser Met Tyr Leu Tyr Cys Asn Leu				
	225		230	235
				240
Gln				

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

GCTCTTTCTC	TCCCTCCTC	TGAATTTAAT	TCTTTCAACT	TGCAATTTGC	AAGGATTACA	60
CATTTCACTG	TGATGTATAT	TGTGTTGCAA	AAAAAAAAAA	GTGTCTTTGT	TTAAAAATTAC	120
TTGGTTTGTG	AATCCATCTT	GCTTTTCCCT	CATTGGAAC	AGTCATTAAC	CCATCTCTGA	180
ACTGGTAGAA	AAACATCTGA	AGAGCTAGTC	TATCAGCATC	TGACAGGTGA	ATTGGATGGT	240
TCTCAGAACC	ATTTACCCA	GACAGCCTGT	TTCTATCCTG	TTTAATAAAT	TAGTTTGGGT	300
TCTCTACATG	CATAACAAAC	CCTGCTCCAA	TCTGTCACAT	AAAAGTCTGT	GACTTGAAGT	360
TTAGTC						366

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

ACAAAGATGA	ACCATTTCCT	ATATTATAGC	AAAATTAAAA	TCTACCCGTA	TTCTAATATT	60
GAGAAATGAG	ATNAAACACA	ATNTTATAAA	GTCTACTTAG	AGAAGATCAA	GTGACCTCAA	120
AGACTTTACT	ATTTTCATAT	TTTAAGACAC	ATGATTTATC	CTATTTTAGT	AACCTGGTTC	180
ATACGTTAAA	CAAAGGATAA	TGTGAACAGC	AGAGAGGATT	TGTTGGCAGA	AAATCTATGT	240
TCAATCTNGA	ACTATCTANA	TCACAGACAT	TTCTATTCTT	TT		282

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

ACACATGTCG	CTTCACTGCC	TTCTTAGATG	CTTCTGGTCA	ACATANAGGA	ACAGGGACCA	60
TATTTATCCT	CCCTCCTGAA	ACAATTGCAA	AATAANACAA	AATATATGAA	ACAATTGCAA	120
AATAAGGCAA	AATATATGAA	ACAACAGGTC	TCGAGATATT	GGAAATCAGT	CAATGAAGGA	180
TACTGATCCC	TGATCACTGT	CCTAATGCAG	GATGTGGGAA	ACAGATGAGG	TCACCTCTGT	240
GACTGCCCCA	GCTTACTGCC	TGTAGAGAGT	TTCTANGCTG	CAGTTCAGAC	AGGGAGAAAT	300
TGGGT						305

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

ACCAAGGTGT NTGAATCTCT GACGTGGGGA TCTCTGATTC CCGCACAATC TGAGTGGAAA	60
AATTCCTGGG T	71

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

ACTCCGGTTG GTGTCAGCAG CACGTGGCAT TGAACATNGC AATGTGGAGC CCAAACCACA	60
GAAAATGGGG TGAAATTGGC CAACTTTCTA TNAACTTATG TTGGCAANTT TGCCACCAAC	120
AGTAAGCTGG CCTTCTAAT AAAAGAAAAT TGAAAGGTTT CTCCTAANC GGAATTAANT	180
AATGGANTCA AGANACTCCC AGGCCTCAGC GT	212

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

ACTCGTTGCA NATCAGGGGC CCCCCAGAGT CACCGTTGCA GGAGTCCTTC TGGTCTTGCC	60
CTCCGCCGGC GCAGAACATG CTGGGGTGGT	90

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

TGTANCGTGA ANACGACAGA NAGGGTTGTC AAAAATGGAG AANCCTTGAA GTCATTTTGA	60
GAATAAGATT TGCTAAAAGA TTTGGGGCTA AAACATGGTT ATTGGGAGAC ATTTCTGAAG	120
ATATNCANGT AAATTANGGA ATGAATTCAT GGTTCCTTTG GGAATTCCTT TACGATNGCC	180
AGCATANACT TCATGTGGGG ATANCAGCTA CCCTTGTA	218

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

TAGGGGTGTA TGCAACTGTA AGGACAAAAA TTGAGACTCA ACTGGCTTAA CCAATAAAGG	60
CATTTGTAG CTCATGGAAC AGGAAGTCGG ATGGTGGGGC ATCTTCAGTG CTGCATGAGT	120
CACCACCCCG GCGGGGTCAT CTGTGCCACA GGTCCCTGTT GACAGTGCGG T	171

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

TGTAGCGTGA AGACNACAGA ATGGTGTGTG CTGTGCTATC CAGGAACACA TTTATTATCA	60
TTATCAANTA TTGTGT	76

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

ACCTTTCCCC AAGGCCAATG TCCTGTGTGC TAACTGGCCG GCTGCAGGAC AGCTGCAATT	60
CAATGTGCTG GGTCAATATGG AGGGGAGGAG ACTCTAAAT AGCCAATTTT ATTCTCTTGG	120
TTAAGATTTG T	131

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

ACTTTATCTA CTGGCTATGA AATAGATGGT GGAAAATTGC GTTACCAACT ATACCACTGG	60
CTTGAAAAAG AGGTGATAGC TCTTCAGAGG ACTTGTGACT TTTGCTCAGA TGCTGAAGAA	120
CTACAGTCTG CATTTGCCAG AAATGAAGAT GAATTTGGAT TAAATGAGGA TGCTGAAGAT	180
TTGCCTCACC AAACAAAAGT GAAACAACCTG AGAGAAAATT TTCAGGAAAA AAGACAGTGG	240
CTCTTGAAGT ATCAGTCACT TTTGAGAATG TTTCTTAGTT ACTGCATACT TCATGGATCC	300
CATGGTGGGG GTCTTGCATC TGTAAGAATG GAATTGATTT TGCTTTTGCA AGAATCTCAG	360
CAGGAAACAT CAGAACCACT ATTTTCTAGC CCTCTGTCAG AGCAAACCTC AGTGCCTCTC	420
CTCTTTGCTT GT	432

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

ACACAACCTTG AATAGTAAAA TAGAAACTGA GCTGAAATTT CTAATTCACCT TTCTAACCAT 60
AGTAAGAATG ATATTTCCCC CCAGGGATCA CCAAATATTT ATAAAAATTT GT 112

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

ACCACGAAAC CACAAACAAG ATGGAAGCAT CAATCCACTT GCCAAGCACA GCAG 54

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

ACCTCATTAG TAATTGTTTT GTTGTTTCAT TTTTCTCTAA TGTCTCCCCT CTACCAGCTC 60
ACCTGAGATA ACAGAATGAA AATGGAAGGA CAGCCAGATT TCTCCTTTGC TCTCTGCTCA 120
TTCTCTCTGA AGTCTAGGTT ACCCATTTTG GGGACCCATT ATAGGCAATA AACACAGTTC 180
CCAAAGCATT TGGACAGTTT CTTGTTGTGT TTTAGAATGG TTTTCCTTTT TCTTAGCCTT 240
TTCCTGCAAA AGGCTCACTC AGTCCCTTGC TTGCTCAGTG GACTGGGCTC CCCAGGGCCT 300
AGGCTGCCTT CTTTTCATG TCC 323

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

ACATACATGT GTGTATATTT TTAAATATCA CTTTGTATC ACTCTGACTT TTTAGCATAC	60
TGAAAACACA CTAACATAAT TTNTGTGAAC CATGATCAGA TACAACCCAA ATCATTCATC	120
TAGCACATTC ATCTGTGATA NAAAGATAGG TGAGTTTCAT TTCCTTCACG TTGGCCAATG	180
GATAAACAAA GT	192

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

CCCTTTTSTA TGGAATGAGT AGACTGTATG TTTGAANATT TANCCACAAC CTCTTTGACA	60
TATAATGACG CAACAAAAAG GTGCTGTTTA GTCCTATGGT TCAGTTTATG CCCCTGACAA	120
GTTTCCATTG TGTTTGGCCG ATCTTCTGGC TAATCGTGGT ATCCTCCATG TTATTAGTAA	180
TTCTGTATTC CATTTTGTTA ACGCCTGGTA GATGTAACCT GCTANGAGGC TAACTTTATA	240
CTTATTTAAA AGCTCTTATT TTGTGGTCAT TAAAATGGCA ATTTATGTGC AGCACTTTAT	300
TGCAGCAGGA AGCACGTGTG GGTGGTGTG AAAGCTCTTT GCTAATCTTA AAAAGTAATG	360
GG	362

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

CTTTTGTAAA GATCGTGTCC ACTCCTGTGG ACATCTTGTT TTAATGGAGT TTCCCATGCA	60
GTANGACTGG TATGGTTGCA GCTGTCCAGA TAAAAACATT TGAAGAGCTC CAAAATGAGA	120
GTTCTCCAG GTTCGCCCTG CTGCTCCAAG TCTCAGCAGC AGCCTCTTTT AGGAGGCATC	180
TTCTGAACTA GATTAAGGCA GCTTGTAAT CTGATGTGAT TTGGTTTATT ATCCAACATA	240
CTTCCATCTG TTATCACTGG AGAAAGCCCA GACTCCCAN GACNGGTACG GATTGTGGGC	300
ATANAAGGAT TGGGTGAAGC TGGCGTTGTG GT	332

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

ACTTTTGCCA TTTTGTATAT ATAAACAATC TTGGGACATT CTCCTGAAAA CTAGGTGTCC	60
AGTGGCTAAG AGAACTCGAT TTCAAGCAAT TCTGAAAGGA AAACCAGCAT GACACAGAAT	120
CTCAAATTCC CAAACAGGGG CTCTGTGGGA AAAATGAGGG AGGACCTTTG TATCTCGGGT	180
TTTAGCAAGT TAAATGAAN ATGACAGGAA AGGCTTATTT ATCAACAAAG AGAAGAGTTG	240
GGATGCTTCT AAAAAAACT TTGGTAGAGA AAATAGGAAT GCTNAATCCT AGGGAAGCCT	300
GTAACAATCT ACAATTGGTC CA	322

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 278 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

ACAAGCCTTC ACAAGTTTAA CTAAATTGGG ATTAATCTTT CTGTANTTAT CTGCATAATT	60
CTTGTTTTTC TTTCCATCTG GCTCCTGGGT TGACAATTTG TGGAAACAAC TCTATTGCTA	120
CTATTTAAAA AAAATCACAA ATCTTTCCT TTAAGCTATG TTNAATTCAA ACTATTCCTG	180
CTATTCCTGT TTTGTCAAAG AAATTATATT TTTCAAATA TGTNTATTG TTTGATGGGT	240
CCCACGAAAC ACTAATAAAA ACCACAGAGA CCAGCCTG	278

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

GTTTANAAAA	CTTGTTTAGC	TCCATAGAGG	AAAGAATGTT	AAACTTTGTA	TTTTAAAACA	60
TGATTCTCTG	AGGTAAACT	TGGTTTTCAA	ATGTTATTTT	TACTTGTATT	TTGCTTTTGG	120
T						121

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

ACTTANAACC	ATGCCTAGCA	CATCAGAATC	CCTCAAAGAA	CATCAGTATA	ATCCTATAACC	60
ATANCAAGTG	GTGACTGGTT	AAGCGTGCGA	CAAAGGTCAG	CTGGCACATT	ACTTGTGTGC	120
AAACTTGATA	CTTTTGTCT	AAGTAGGAAC	TAGTATACAG	TNCCTAGGAN	TGGTACTCCA	180
GGGTGCCCCC	CAACTCCTGC	AGCCGCTCCT	CTGTGCCAGN	CCCTGNAAGG	AACTTTCGCT	240
CCACCTCAAT	CAAGCCCTGG	GCCATGCTAC	CTGCAATTGG	CTGAACAAAC	GTTTGCTGAG	300
TTCCCAAGGA	TGCAAAACCT	GGTGCTCAAC	TCCTGGGGCG	TCAACTCAGT		350

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

TGTACCGTGA	AGACGACAGA	AGTTGCATGG	CAGGGACAGG	GCAGGGCCGA	GGCCAGGGTT	60
GCTGTGATTG	TATCCGAATA	NTCCTCGTGA	GAAAAGATAA	TGAGATGACG	TGAGCAGCCT	120
GCAGACTTGT	GTCTGCCTTC	AANAAGCCAG	ACAGGAAGGC	CCTGCCTGCC	TTGGCTCTGA	180
CCTGGCGGCC	AGCCAGCCAG	CCACAGGTGG	GCTTCTTCCT	TTTGTGGTGA	CAACNCCAAG	240
AAAACCTGCAG	AGGCCCAGGG	TCAGGTGTNA	GTGGGTANGT	GACCATAAAA	CACCAGGTGC	300
TCCCAGGAAC	CCGGGCAAAG	GCCATCCCCA	CCTACAGCCA	GCATGCCAC	TGGCGTGATG	360
GGTGCAAG	GATGAAGCAG	CCAGNTGTTC	TGCTGTGGT			399

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

ACTGGTGTGG	TNGGGGGTGA	TGCTGGTGGT	ANAAGTTGAN	GTGACTTCAN	GATGGTGTGT	60
GGAGGAAGTG	TGTGAACGTA	GGGATGTAGA	NGTTTTGGCC	GTGCTAAATG	AGCTTCGGGA	120
TTGGCTGGTC	CCACTGGTGG	TCACTGTCAT	TGGTGGGGTT	CCTGT		165

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 338 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

ACTCACTGGA	ATGCCACATT	CACAACAGAA	TCAGAGGTCT	GTGAAAACAT	TAATGGCTCC	60
TTAACTTCTC	CAGTAAGAAT	CAGGGACTTG	AAATGGAAAC	GTTAACAGCC	ACATGCCCAA	120
TGCTGGGCAG	TCTCCCATGC	CTTCCACAGT	GAAAGGGCTT	GAGAAAAATC	ACATCCAATG	180
TCATGTGTTT	CCAGCCACAC	CAAAAGGTGC	TTGGGGTGGA	GGGCTGGGGG	CATANANGGT	240
CANGCCTCAG	GAAGCCTCAA	GTTCCATTCA	GCTTTGCCAC	TGTACATTCC	CCATNTTTAA	300
AAAACTGAT	GCCTTTTTTT	TTTTTTTTTG	TAAAAATTC			338

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 382 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

GGGAATCTTG	GTTTTTGGCA	TCTGGTTTGC	CTATAGCCGA	GGCCACTTTG	ACAGAACAAA	60
GAAAGGGACT	TCGAGTAAGA	AGGTGATTTA	CAGCCAGCCT	AGTGCCCGAA	GTGAAGGAGA	120
ATTCAAACAG	ACCTCGTCAT	TCCTGGTGTG	AGCCTGGTCG	GCTCACCGCC	TATCATCTGC	180

100

ATTTGCCTTA	CTCAGGTGCT	ACCGGACTCT	GGCCCCTGAT	GTCTGTAGTT	TCACAGGATG	240
CCTTATTTGT	CTTCTACACC	CCACAGGGCC	CCCTACTTCT	TCGGATGTGT	TTTTAATAAT	300
GTCAGCTATG	TGCCCCATCC	TCCTTCATGC	CCTCCCTCCC	TTTCCTACCA	CTGCTGAGTG	360
GCCTGGAAGT	TGTTTAAAGT	GT				382

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

ACCAAANCTT	CTTCTGTTG	TGTTNGATTT	TACTATAGGG	GTTTNGCTTN	TTCTAAANAT	60
ACTTTTCATT	TAAACNCTTT	TGTTAAGTGT	CAGGCTGCAC	TTTGCTCCAT	ANAATTATTG	120
TTTTCACATT	TCAACTTGTA	TGTGTTTGTC	TCTTANAGCA	TTGGTGAAAT	CACATATTTT	180
ATATTCAGCA	TAAAGGAGAA					200

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

ACTTTATTTT	CAAAACACTC	ATATGTTGCA	AAAAACACAT	AGAAAAATAA	AGTTTGGTGG	60
GGTGCTGAC	TAAACTTCAA	GTACAGACT	TTTATGTGAC	AGATTGGAGC	AGGGTTTGTT	120
ATGCATGTAG	AGAACCCAAA	CTAATTTATT	AAACAGGATA	GAAACAGGCT	GTCTGGGTGA	180
AATGGTTCTG	AGAACCATCC	AATTCACCTG	TCAGATGCTG	ATANACTAGC	TCTTCAGATG	240
TTTTTCTACC	AGTTCAGAGA	TNGGTTAATG	ACTANTTCCA	ATGGGGAAAA	AGCAAGATGG	300
ATTCACAAAC	CAAGTAATTT	TAAACAAAGA	CACCTT			335

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 459 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

ACCAGGTAA TATTGCCACA TATATCCTTT CCAATTGCGG GCTAAACAGA CGTGTATTTA	60
GGGTTGTTA AAGACAACCC AGCTTAATAT CAAGAGAAAT TGTGACCTTT CATGGAGTAT	120
CTGATGGAGA AAACACTGAG TTTTGACAAA TCTTATTTTA TTCAGATAGC AGTCTGATCA	180
CACATGGTCC AACAACTCTC AAATAATAAA TCAAATATNA TCAGATGTTA AAGATTGGTC	240
TTCAAACATC ATAGCCAATG ATGCCCCGCT TGCCTATAAT CTCTCCGACA TAAAACCACA	300
TCAACACCTC AGTGGCCACC AAACCATTCA GCACAGCTTC CTTAACTGTG AGCTGTTTGA	360
AGCTACCACT CTGAGCACTA TTGACTATNT TTTTCANGCT CTGAATAGCT CTAGGGATCT	420
CAGCANGGGT GGGAGGAACC AGCTCAACCT TGGCGTANT	459

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 140 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

ACATTTCTT CCACCAAGTC AGGACTCCTG GCTTCTGTGG GAGTTCTTAT CACCTGAGGG	60
AAATCCAAAC AGTCTCTCCT AGAAAGGAAT AGTGTCACCA ACCCCACCCA TCTCCCTGAG	120
ACCATCCGAC TTCCCTGTGT	140

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 164 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

ACTTCAGTAA CAACATACAA TAACAACATT AAGTGATAT TGCCATCTTT GTCATTTTCT	60
ATCTATACCA CTCTCCCTTC TGAAAACAAN AATCACTANC CAATCACTTA TACAAATTTG	120
AGGCAATTAA TCCATATTTG TTTTCAATAA GGAAAAAAG ATGT	164

(2) INFORMATION FOR SEQ ID NO:145:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 303 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

ACGTAGACCA	TCCAACTTG	TATTTGTAAT	GGCAAACATC	CAGNAGCAAT	TCCTAAACAA	60
ACTGGAGGGT	ATTTATACCC	AATTATCCCA	TTCATTAACA	TGCCCTCCTC	CTCAGGCTAT	120
GCAGGACAGC	TATCATAAGT	CGGCCCAGGC	ATCCAGATAC	TACCATTTGT	ATAAACTTCA	180
GTAGGGGAGT	CCATCCAAGT	GACAGGTCTA	ATCAAAGGAG	GAAATGGAAC	ATAAGCCCAG	240
TAGTAAATN	TTGCTTAGCT	GAAACAGCCA	CAAAGACTT	ACCGCCGTGG	TGATTACCAT	300
CAA						303

(2) INFORMATION FOR SEQ ID NO:146:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 327 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

ACTGCAGCTC	AATTAGAAGT	GGTCTCTGAC	TTTCATCANC	TTCTCCCTGG	GCTCCATGAC	60
ACTGGCCTGG	AGTGACTCAT	TGCTCTGGTT	GGTTGAGAGA	GCTCCTTTGC	CAACAGGCCT	120
CCAAGTCAGG	GCTGGGATTT	GTTTCCTTTC	CACATTCTAG	CAACAATATG	CTGGCCACTT	180
CCTGAACAGG	GAGGGTGGGA	GGAGCCAGCA	TGGAACAAGC	TGCCACTTTC	TAAAGTAGCC	240
AGACTTGCCC	CTGGGCCTGT	CACACCTACT	GATGACCTTC	TGTGCCTGCA	GGATGGAATG	300
TAGGGGTGAG	CTGTGTGACT	CTATGGT				327

(2) INFORMATION FOR SEQ ID NO:147:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 173 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

ACATTGTTTT TTTGAGATAA AGCATTGANA GAGCTCTCCT TAACGTGACA CAATGGAAGG	60
ACTGGAACAC ATACCCACAT CTTTGTTCCTG AGGGATAATT TTCTGATAAA GTCTTGCTGT	120
ATATTCAAGC ACATATGTTA TATATTATTC AGTTCCATGT TTATAGCCTA GTT	173

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

ACAACCACTT TATCTCATCG AATTTTAAAC CCAAACCTCAC TCACTGTGCC TTTCTATCCT	60
ATGGGATATA TTATTTGATG CTCCATTTC AATCACATAT ATGAATAATA CACTCATACT	120
GCCCTACTAC CTGCTGCAAT AATCACATTC CCTTCCTGTC CTGACCCTGA AGCCATTGGG	180
GTGGTCCTAG TGGCCATCAG TCCANGCCTG CACCTTGAGC CCTTGAGCTC CATTGCTCAC	240
NCCANCCAC CTCACCGACC CCATCCTCTT ACACAGCTAC CTCCTTGCTC TCTAACCCCA	300
TAGATTATNT CCAAATTCAG TCAATTAAGT TACTATTAAC ACTCTACCCG ACATGTCCAG	360
CACCACTGGT AAGCCTTCTC CAGCCAACAC ACACACACAC ACACNCACAC ACACACATAT	420
CCAGGCACAG GCTACCTCAT CTTACAATC ACCCCTTTAA TTACCATGCT ATGGTGG	477

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

ACAGTTGTAT TATAATATCA AGAAATAAAC TTGCAATGAG AGCATTTAAG AGGGAAGAAC	60
TAACGTATTT TAGAGAGCCA AGGAAGGTTT CTGTGGGGAG TGGGATGTAA GGTGGGGCCT	120
GATGATAAAT AAGAGTCAGC CAGGTAAGTG GGTGGTGTGG TATGGGCACA GTGAAGAACA	180
TTTCAGGCAG AGGGAACAGC AGTGAAA	207

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs

104

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

```
ACCTTGATTT CATTGCTGCT CTGATGGAAA CCCAACTATC TAATTTAGCT AAAACATGGG      60
CACTTAAATG TGGTCAGTGT TTGGACTTGT TAACTANTGG CATCTTTGGG T                111
```

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

```
AGCGCGGCAG GTCATATTGA ACATTCCAGA TACCTATCAT TACTCGATGC TGTGATAAC      60
AGCAAGATGG CTTTGAAGTC AGGGTCACCA CCAGCTATTG GACCTTACTA TGAAAACCAT      120
GGATACCAAC CGGAAAACCC CTATCCCGCA CAGCCCACTG TGGTCCCCAC TGTCTACGAG      180
GTGCATCCGG CTCAGT                                     196
```

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

```
ACAGCACTTT CACATGTAAG AAGGGAGAAA TTCCTAAATG TAGGAGAAAG ATAACAGAAC      60
CTTCCCCTTT TCATCTAGTG GTGGAAACCT GATGCTTTAT GTTGACAGGA ATAGAACCAG      120
GAGGGAGTTT GT                                         132
```

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

ACAAACCCCA	NGANAGGCCA	CTGGCCGTGG	TGTCATGGCC	TCCAAACATG	AAAGTGTCTAG	60
CTTCTGCTCT	TATGTCCTCA	TCTGACAAC	CTTTACCATT	TTATCCTCG	CTCAGCAGGA	120
GCACATCAAT	AAAGTCCAAA	GTCTTGGA	TGGCCTTGGC	TTGGAGGAAG	TCATCAACAC	180
CCTGGCTAGT	GAGGGTGCGG	CGCCGCTCCT	GGATGACGGC	ATCTGTGAAG	TCGTGCACCA	240
GTCTGCAGGC	CCTGTGGAAG	CGCCGTCCAC	ACGGAGTNAG	GAATT		285

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

ACCACAGTCC	TGTTGGGCCA	GGGCTTCATG	ACCCTTTCTG	TGAAAAGCCA	TATTATCACC	60
ACCCCAAATT	TTTCCTTAAA	TATCTTTAAC	TGAAGGGGTC	AGCCTCTTGA	CTGCAAAGAC	120
CCTAAGCCGG	TTACACAGCT	AACTCCCACT	GGCCCTGATT	TGTGAAATTG	CTGCTGCCTG	180
ATTGGCACAG	GAGTCGAAGG	TGTTCAAGCTC	CCCTCCTCCG	TGGAACGAGA	CTCTGATTTG	240
AGTTTCACAA	ATTCTCGGGC	CACCTCGTCA	TGCTCCTCT	GAAATAAAAT	CCGGAGAATG	300
GTCAGGCCTG	TCTCATCCAT	ATGGATCTTC	CGG			333

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

```

ACTGGAAATA ATAAAACCCA CATCACAGTG TTGTGTCAAA GATCATCAGG GCATGGATGG      60
GAAAGTGCTT TGGGAAGTGT AAAGTGCCTA ACACATGATC GATGATTTT GTTATAATAT      120
TTGAATCACG GTGCATACAA ACTCTCCTGC CTGCTCCTCC TGGGCCCCAG CCCCAGCCCC      180
ATCACAGCTC ACTGCTCTGT TCATCCAGGC CCAGCATGTA GTGGCTGATT CTTCTTGGCT      240
GCTTTTAGCC TCCANAAGTT TCTCTGAAGC CAACCAAACC TCTANGTGTA AGGCATGCTG      300
GCCCTGGT                                     308

```

(2) INFORMATION FOR SEQ ID NO:156:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 295 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

```

ACCTTGCTCG GTGCTTGGA CATATTAGGA ACTCAAATA TGAGATGATA ACAGTGCCTA      60
TTATTGATTA CTGAGAGAAC TGTTAGACAT TTAGTTGAAG ATTTTCTACA CAGGAAGTGA      120
GAATAGGAGA TTATGTTTGG CCCTCATATT CTCTCCTATC CTCCTTGCCT CATTCTATGT      180
CTAATATATT CTCAATCAA TAAGGTTAGC ATAATCAGGA AATCGACCAA ATACCAATAT      240
AAAACCAGAT GTCTATCCTT AAGATTTTCA AATAGAAAAC AAATTAACAG ACTAT          295

```

(2) INFORMATION FOR SEQ ID NO:157:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 126 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

```

ACAAGTTTAA ATAGTGCTGT CACTGTGCAT GTGCTGAAAT GTGAAATCCA CCACATTTCT      60
GAAGAGCAAAA ACAAATTCTG TCATGTAATC TCTATCTTGG GTCGTGGGTA TATCTGTCCC      120
CTTAGT                                     126

```

(2) INFORMATION FOR SEQ ID NO:158:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 442 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

ACCCACTGGT	CTTGAAACA	CCCATCCTTA	ATACGATGAT	TTTCTGTCTG	TGTGAAAATG	60
AANCCAGCAG	GCTGCCCCTA	GTCAGTCCTT	CCTTCAGAG	AAAAAGAGAT	TTGAGAAAGT	120
GCCTGGGTAA	TTCACCATTA	ATTTCCTCCC	CCAAACTCTC	TGAGTCTTCC	CTTAATATTT	180
CTGGTGGTTC	TGACCAAAGC	AGGTCATGGT	TTGTTGAGCA	TTGGGGATCC	CAGTGAAGTA	240
NATGTTTGTA	GCCTTGCCATA	CTTAGCCCTT	CCCACGCACA	AACGGAGTGG	CAGAGTGGTG	300
CCAACCTGT	TTTCCAGTC	CACGTAGACA	GATTCACAGT	GCGGAATTCT	GGAAGCTGGA	360
NACAGACGGG	CTCTTTGCAG	AGCCGGGACT	CTGAGANGGA	CATGAGGGCC	TCTGCCTCTG	420
TGTTCACTCT	CTGATGTCCT	GT				442

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 498 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

ACTTCCAGGT	AACGTTGTTG	TTTCCGTTGA	GCCTGAACTG	ATGGGTGACG	TTGTAGGTTT	60
TCCAACAAGA	ACTGAGGTTG	CAGAGCGGGT	AGGGAAGAGT	GCTGTTCCAG	TTGCACCTGG	120
GCTGCTGTGG	ACTGTTGTTG	ATTCTCACT	ACGGCCCAAG	GTTGTGGAAC	TGGCANAAAG	180
GTGTGTTGTT	GGANTTGAGC	TCGGGCGGCT	GTGGTAGGTT	GTGGGCTCTT	CAACAGGGGC	240
TGCTGTGGTG	CCGGGANGTG	AANGTGTTGT	GTCACCTGAG	CTTGCCAGC	TCTGGAAGT	300
ANTANATTCT	TCCTGAAGGC	CAGCGCTTGT	GGAGCTGGCA	NGGGTCANTG	TTGTGTGTAA	360
CGAACCAGTG	CTGCTGTGGG	TGGGTGTANA	TCCTCCACAA	AGCCTGAAGT	TATGGTGTCN	420
TCAGGTAANA	ATGTGGTTTC	AGTGTCCCTG	GGCNGCTGTG	GAAGGTTGTA	NATTGTCACC	480
AAGGAATAA	GCTGTGGT					498

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 380 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

ACCTGCATCC	AGCTTCCCTG	CCAAACTCAC	AAGGAGACAT	CAACCTCTAG	ACAGGGAAAC	60
AGCTTCAGGA	TACTTCCAGG	AGACAGAGCC	ACCAGCAGCA	AAACAAATAT	TCCCATGCCT	120
GGAGCATGGC	ATAGAGGAAG	CTGANAAATG	TGGGGTCTGA	GGAAGCCATT	TGAGTCTGGC	180
CACTAGACAT	CTCATCAGCC	ACTTGTGTGA	AGAGATGCCC	CATGACCCCA	GATGCCTCTC	240
CCACCCTTAC	CTCCATCTCA	CACACTTGAG	CTTTCCACTC	TGTATAATTC	TAACATCCTG	300
GAGAAAAATG	GCAGTTTGAC	CGAACCTGTT	CACAACGGTA	GAGGCTGATT	TCTAACGAAA	360
CTTGTAGAAT	GAAGCCTGGA					380

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

ACTCCACATC	CCCTCTGAGC	AGGCGGTTGT	CGTTCAAGGT	GTATTTGGCC	TTGCCTGTCA	60
CACTGTCCAC	TGGCCCTTA	TCCACTTGGT	GCTTAATCCC	TCGAAAGAGC	ATGT	114

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

ACTTTCTGAA	TCGAATCAAA	TGATACTTAG	TGTAGTTTTA	ATATCCTCAT	ATATATCAAA	60
GTTTTACTAC	TCTGATAATT	TTGTAAACCA	GGTAACCAGA	ACATCCAGTC	ATACAGCTTT	120
TGGTGATATA	TAACCTGGCA	ATAACCCAGT	CTGGTGATAC	ATAAACTAC	TCACTGT	177

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

CATTTATACA GACAGGCGTG AAGACATTCA CGACAAAAC GCGAAATTCT ATCCCGTGAC	60
CANAGAAGGC AGCTACGGCT ACTCCTACAT CCTGGCGTGG GTGGCCTTCG CCTGCACCTT	120
CATCAGCGGC ATGATGT	137

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 469 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

CTTATCACAA TGAATGTTCT CCTGGGCAGC GTTGTGATCT TTGCCACCTT CGTGACTTTA	60
TGCAATGCAT CATGCTATTT CATACTAAT GAGGGAGTTC CAGGAGATTC AACCAGGAAA	120
TGCATGGATC TCAAAGGAAA CAAACACCCA ATAACTCGG AGTGGCAGAC TGACAACTGT	180
GAGACATGCA CTTGCTACGA AACAGAAATT TCATGTTGCA CCCTTGTTTC TACACCTGTG	240
GGTTATGACA AAGACAACCTG CCAAGAATC TTCAAGAAGG AGGACTGCAA GTATATCGTG	300
GTGGAGAAGA AGGACCCAAA AAAGACCTGT TCTGTCAGTG AATGGATAAT CTAATGTGCT	360
TCTAGTAGGC ACAGGGCTCC CAGGCCAGGC CTCATTCTCC TCTGGCCTCT AATAGTCAAT	420
GATTGTGTAG CCATGCCTAT CAGTAAAAG ATNTTTGAGC AAACACTTT	469

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 195 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

ACAGTTTTTT ATANATATCG ACATTGCCGG CACTTGTGTT CAGTTTCATA AAGCTGGTGG	60
ATCCGCTGTC ATCCACTATT CCTTGGCTAG AGTAAAAATT ATTCTTATAG CCCATGTCCC	120
TGCAGGCCGC CCGCCCGTAG TTCTCGTTCC AGTCGTCTTG GCACACAGGG TGCCAGGACT	180
TCCTCTGAGA TGAGT	195

(2) INFORMATION FOR SEQ ID NO:166:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 383 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

ACATCTTAGT AGTGTGGCAC ATCAGGGGGC CATCAGGGTC ACAGTCACTC ATAGCCTCGC	60
CGAGGTCCGA GTCCACACCA CCGGTGTAGG TGTGCTCAAT CTTGGGCTTG GCGCCACCT	120
TTGGAGAAGG GATATGCTGC ACACACATGT CCACAAAGCC TGTGAACTCG CCAAAGAATT	180
TTTGCAGACC AGCCTGAGCA AGGGGCGGAT GTTCAGCTTC AGCTCCTCCT TCGTCAGGTG	240
GATGCCAACC TCGTCTANGG TCCGTGGGAA GCTGGTGTCC ACNTCACCTA CAACCTGGGC	300
GANGATCTTA TAAAGAGGCT CCNAGATAAA CTCCACGAAA CTTCTCTGGG AGCTGCTAGT	360
NGGGGCCTTT TTGGTGAAC TTC	383

(2) INFORMATION FOR SEQ ID NO:167:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 247 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

ACAGAGCCAG ACCTTGGCCA TAAATGAANC AGAGATTAAG ACTAAACCCC AAGTCGANAT	60
TGGAGCAGAA ACTGGAGCAA GAAGTGGGCC TGGGGCTGAA GTAGAGACCA AGGCCACTGC	120
TATANCCATA CACAGAGCCA ACTCTCAGGC CAAGGCNATG GTTGGGGCAG ANCCAGAGAC	180
TCAATCTGAN TCCAAAGTGG TGGCTGGAAC ACTGGTCATG ACANAGGCAG TGACTCTGAC	240
TGANGTC	247

(2) INFORMATION FOR SEQ ID NO:168:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 273 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

ACTTCTAAGT TTTCTAGAAG TGGAAGGATT GTANTCATCC TGAAAATGGG TTTACTTCAA	60
AATCCCTCAN CCTTGTTCTT CACNACTGTC TATACTGANA GTGTCATGTT TCCACAAAGG	120
GCTGACACCT GAGCCTGNAT TTTCACTCAT CCCTGAGAAG CCCTTTCCAG TAGGGTGGGC	180
AATTCCCAAC TTCCTTGCCA CAAGCTTCCC AGGCTTTCTC CCCTGGAAAA CTCCAGCTTG	240
AGTCCCAGAT ACACTCATGG GCTGCCCTGG GCA	273

(2) INFORMATION FOR SEQ ID NO:169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 431 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

ACAGCCTTGG CTTCCCCAAA CTCCACAGTC TCAGTGCAGA AAGATCATCT TCCAGCAGTC	60
AGCTCAGACC AGGGTCAAAG GATGTGACAT CAACAGTTTC TGGTTTCAGA ACAGGTTCTA	120
CTACTGTCAA ATGACCCCCC ATAATTCTC AAAGGCTGTG GTAAGTTTGT CACAGGTGAG	180
GGCAGCAGAA AGGGGGTANT TACTGATGGA CACCATCTTC TCTGTATACT CCACACTGAC	240
CTTGCCATGG GCAAAGGCC CTACCACAAA AACAATAGGA TCACTGCTGG GCACCAGCTC	300
ACGCACATCA CTGACAACCG GGATGGAAAA AGAANTGCCA ACTTTCATAC ATCCAAGTGG	360
AAAGTGATCT GATACTGGAT TCTTAATTAC CTTCAAAAGC TTCTGGGGGC CATCAGCTGC	420
TCGAACACTG A	431

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

ACCTGTGGGC TGGGCTGTTA TGCCTGTGCC GGCTGCTGAA AGGGAGTTCA GAGGTGGAGC	60
TCAAGGAGCT CTGCAGGCAT TTTGCCAANC CTCTCCANAG CANAGGGAGC AACCTACACT	120
CCCCGCTAGA AAGACACCAG ATTGGAGTCC TGGGAGGGGG AGTTGGGGTG GGCATTTGAT	180
GTATACTTGT CACCTGAATG AANGAGCCAG AGAGGAANGA GACGAANATG ANATTGGCCT	240
TCAAAGCTAG GGGTCTGGCA GGTGGA	266

(2) INFORMATION FOR SEQ ID NO:171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1248 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

GGCAGCCAAA TCATAAACGG CGAGGACTGC AGCCCGCACT CGCAGCCCTG GCAGGCGGCA	60
CTGGTCATGG AAAACGAATT GTTCTGCTCG GCGCTCCTGG TGCATCCGCA GTGGGTGCTG	120
TCAGCCGCAC ACTGTTTCCA GAAGTGAGTG CAGAGCTCCT ACACCATCGG GCTGGGCCTG	180
CACAGTCTTG AGGCCGACCA AGAGCCAGGG AGCCAGATGG TGGAGGCCAG CCTCTCCGTA	240
CGGCACCCAG AGTACAACAG ACCCTTGCTC GCTAACGACC TCATGCTCAT CAAGTTGGAC	300
GAATCCGTGT CCGAGTCTGA CACCATCCGG AGCATCAGCA TTGCTTCGCA GTGCCCTACC	360
GCGGGGAACT CTTGCCTCGT TTCTGGCTGG GGTCTGCTGG CGAACGGCAG AATGCCTACC	420
GTGCTGCACT GCGTGAACGT GTCGGTGGTG TCTGAGGAGG TCTGCAGTAA GCTCTATGAC	480
CCGCTGTACC ACCCCAGCAT GTTCTGCGCC GCGCGAGGGC AAGACCAGAA GGACTCCTGC	540
AACGGTGACT CTGGGGGGCC CCTGATCTGC AACGGTACT TGCAGGGCCT TGTGTCTTTC	600
GGAAAAGCCC CGTGTGGCCA AGTTGGCGTG CCAGGTGTCT ACACCAACCT CTGCAAATTC	660
ACTGAGTGGA TAGAGAAAAC CGTCCAGGCC AGTTAACTCT GGGGACTGGG AACCCATGAA	720
ATTGACCCCC AAATACATCC TGCGGAAGGA ATTCAGGAAT ATCTGTTCCC AGCCCCCTCT	780
CCCTCAGGCC CAGGAGTCCA GGCCCCCAGC CCCTCCTCCC TCAAACCAAG GGTACAGATC	840
CCCAGCCCCT CCTCCCTCAG ACCCAGGAGT CCAGACCCCC CAGCCCCCTCC TCCCTCAGAC	900
CCAGGAGTCC AGCCCCCTCT CCCTCAGACC CAGGAGTCCA GACCCCCCAG CCCCTCCTCC	960
CTCAGACCCA GGGGTCCAGG CCCCCAACCC CTCCTCCCTC AGACTCAGAG GTCCAAGCCC	1020
CCAACCCNTC ATTCCCCAGA CCCAGAGGTC CAGGTCCCAG CCCCTCNTCC CTCAGACCCA	1080
GCGGTCCAAT GCCACCTAGA CTNTCCCTGT ACACAGTGCC CCCTTGTTGGC ACGTTGACCC	1140
AACCTTACCA GTTGGTTTTT CATTTTNGT CCCTTTCCCC TAGATCCAGA AATAAAGTTT	1200
AAGAGAAGNG CAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	1248

(2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

Met	Val	Glu	Ala	Ser	Leu	Ser	Val	Arg	His	Pro	Glu	Tyr	Asn	Arg	Pro
1					5				10					15	

Leu Leu Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser
 20 25 30
 Glu Ser Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr
 35 40 45
 Ala Gly Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly
 50 55 60
 Arg Met Pro Thr Val Leu Gln Cys Val Asn Val Ser Val Val Ser Glu
 65 70 75 80
 Glu Val Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe
 85 90 95
 Cys Ala Gly Gly Gly Gln Xaa Gln Xaa Asp Ser Cys Asn Gly Asp Ser
 100 105 110
 Gly Gly Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe
 115 120 125
 Gly Lys Ala Pro Cys Gly Gln Val Gly Val Pro Gly Val Tyr Thr Asn
 130 135 140
 Leu Cys Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Ala Ser
 145 150 155

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1265 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

GGCAGCCCGC	ACTCGCAGCC	CTGGCAGGCG	GCACTGGTCA	TGGAAAACGA	ATTGTTCTGC	60
TCGGGCGTCC	TGGTGCAATC	GCACTGGGTC	CTGTCAGCCG	CACACTGTTT	CCAGAACTCC	120
TACACCATCG	GGCTGGGCCT	GCACAGTCTT	GAGGCCGACC	AAGAGCCAGG	GAGCCAGATG	180
GTGGAGGCCA	GCCTCTCCGT	ACGGCACCCA	GAGTACAACA	GACCCTTGCT	CGCTAACGAC	240
CTCATGCTCA	TCAAGTTGGA	CGAATCCGTG	TCCGAGTCTG	ACACCATCCG	GAGCATCAGC	300
ATTGCTTCGC	AGTGCCCTAC	CGCGGGGAAC	TCTTGCCCTG	TTTCTGGCTG	GGGTCTGCTG	360
GCGAACGGTG	AGCTCACGGG	TGTGTGCTCT	CCCTCTTCAA	GGAGGTCCTC	TGCCCCAGTCG	420
CGGGGGGTGA	CCCAGAGCTC	TGCGTCCCAG	GCAGAATGCC	TACCGTGCTG	CAGTGCGTGA	480
ACGTGTCGGT	GGTGTCTGAG	GAGGTCTGCA	GTAAGCTCTA	TGACCCGCTG	TACCACCCCA	540
GCACTGTTCT	CGCCGGCGGA	GGGCAAGACC	AGAAGGACTC	CTGCAACGGT	GACTCTGGGG	600
GGCCCCTGAT	CTGCAACGGG	TACTTGCAGG	GCCTTGTGTC	TTTCGGAAAA	GCCCCGTGTG	660
GCCAAGTTGG	CGTGCCAGGT	GTCTACACCA	ACCTCTGCAA	ATTCAGTGA	TGGATAGAGA	720

AAACCGTCCA	GGCCAGTTAA	CTCTGGGGAC	TGGGAACCCA	TGAAATTGAC	CCCCAAATAC	780
ATCCTGCGGA	AGGAATTCTAG	GAATATCTGT	TCCCAGCCCC	TCCTCCCTCA	GGCCCAGGAG	840
TCCAGGCCCC	CAGCCCCTCC	TCCCTCAAAC	CAAGGGTACA	GATCCCCAGC	CCCTCCTCCC	900
TCAGACCCAG	GAGTCCAGAC	CCCCCAGCCC	CTCCTCCCTC	AGACCCAGGA	GTCCAGCCCC	960
TCCTCCNTCA	GACCCAGGAG	TCCAGACCCC	CCAGCCCCCTC	CTCCCTCAGA	CCCAGGGGTT	1020
GAGGCCCCCA	ACCCCTCCTC	CTTCAGAGTC	AGAGGTCCAA	GCCCCCAACC	CCTCGTTCCC	1080
CAGACCCAGA	GGTNNAGGTC	CCAGCCCCCTC	TTCCNTCAGA	CCCAGNGGTC	CAATGCCACC	1140
TAGATTTTCC	CTGNACACAG	TGCCCCCTTG	TGGNANGTTG	ACCCAACCTT	ACCAGTTGGT	1200
TTTTCATTTT	TNGTCCCTTT	CCCCTAGATC	CAGAAATAAA	GTTTAAGAGA	NGNGCAAAAA	1260
AAAAA						1265

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1459 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

GGTCAGCCGC	ACACTGTTTC	CAGAAGTGAG	TGCAGAGCTC	CTACACCATC	GGGCTGGGCC	60
TGCACAGTCT	TGAGGCCGAC	CAAGAGCCAG	GGAGCCAGAT	GGTGGAGGCC	AGCCTCTCCG	120
TACGGCACCC	AGAGTACAAC	AGACCCTTGC	TCGCTAACGA	CCTCATGCTC	ATCAAGTTGG	180
ACGAATCCGT	GTCCGAGTCT	GACACCATCC	GGAGCATCAG	CATTGCTTCG	CAGTGCCTTA	240
CCGCGGGGAA	CTCTTGCCCTC	GTTTCTGGCT	GGGGTCTGCT	GGCGAACGGT	GAGCTCACGG	300
GTGTGTGTCT	GCCCTCTTCA	AGGAGGTCCT	CTGCCCAGTC	GCGGGGGCTG	ACCCAGAGCT	360
CTGCGTCCCA	GGCAGAATGC	CTACCGTGCT	GCAGTGCGTG	AACGTGTCGG	TGGTGTCTGA	420
NGAGGTCTGC	ANTAAGCTCT	ATGACCCGCT	GTACCACCCC	ANCATGTTCT	GCGCCGGCGG	480
AGGGCAAGAC	CAGAAGGACT	CCTGCAACGT	GAGAGAGGGG	AAAGGGGAGG	GCAGGCGACT	540
CAGGGAAGGG	TGGAGAAGGG	GGAGACAGAG	ACACACAGGG	CCGCATGGCG	AGATGCAGAG	600
ATGGAGAGAC	ACACAGGGAG	ACAGTGACAA	CTAGAGAGAG	AAACTGAGAG	AAACAGAGAA	660
ATAAACACAG	GAATAAAGAG	AAGCAAAGGA	AGAGAGAAAC	AGAAACAGAC	ATGGGGAGGC	720
AGAAACACAC	ACACATAGAA	ATGCAGTTGA	CCTTCCAACA	GCATGGGGCC	TGAGGGCGGT	780
GACCTCCACC	CAATAGAAAA	TCCTCTTATA	ACTTTTGACT	CCCCAAAAAC	CTGACTAGAA	840
ATAGCCTACT	GTTGACGGGG	AGCCTTACCA	ATAACATAAA	TAGTCGATT	ATGCATACGT	900
TTTATGCATT	CATGATATAC	CTTTGTTGGA	ATTTTGTGAT	ATTTCTAAGC	TACACAGTTC	960
GTCTGTGAAT	TTTTTTTAAAT	TGTTGCAACT	CTCCTAAAAT	TTTTCTGATG	TGTTTATTGA	1020
AAAAATCCAA	GTATAAGTGG	ACTTGTGCAT	TCAAACCAGG	GTTGTTCAAG	GGTCAACTGT	1080
GTACCCAGAG	GGAAACAGTG	ACACAGATTC	ATAGAGGTGA	AACACGAAGA	GAAACAGGAA	1140
AAATCAAGAC	TCTACAAAGA	GGCTGGGCAG	GGTGGCTCAT	GCCTGTAATC	CCAGCACTTT	1200
GGGAGGCGAG	GCAGGCAGAT	CACTTGAGGT	AAGGAGTTCA	AGACCAGCCT	GGCCAAAATG	1260
GTGAAATCCT	GTCTGTACTA	AAAATACAAA	AGTTAGCTGG	ATATGGTGGC	AGGCGCCTGT	1320
AATCCCAGCT	ACTTGGGAGG	CTGAGGCAGG	AGAATTGCTT	GAATATGGGA	GGCAGAGGTT	1380
GAAGTGAGTT	GAGATCAAC	CACATATCTC	CAGCTGGGGC	AACAGAGTAA	GACTCTGTCT	1440
CAAAAAA	AAAAA					1459

(2) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:

115

- (A) LENGTH: 1167 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

```

GCGCAGCCCT GGCAGGCGGC ACTGGTCATG GAAAACGAAT TGTTCTGCTC GGGCGTCCTG      60
GTGCATCCGC AGTGGGTGCT GTCAGCCGCA CACTGTTTCC AGAACTCCTA CACCATCGGG      120
CTGGGCCTGC ACAGTCTTGA GGCCGACCAA GAGCCAGGGA GCCAGATGGT GGAGGCCAGC      180
CTCTCCGTAC GGCACCCAGA GTACAACAGA CTCTTGCTCG CTAACGACCT CATGCTCATC      240
AAGTTGGACG AATCCGTGTC CGAGTCTGAC ACCATCCGGA GCATCAGCAT TGCTTCGCAG      300
TGCCCTACCG CGGGGAACTC TTGCCCTCGT TCTGGCTGGG GTCTGCTGGC GAACGGCAGA      360
ATGCCTACCG TGCTGCACTG CGTGAACGTG TCGGTGGTGT CTGAGGANGT CTGCAGTAAG      420
CTCTATGACC CGCTGTACCA CCCCAGCATG TTCTGCGCCG GCGGAGGGCA AGACCAGAAG      480
GACTCCTGCA ACGGTGACTC TGGGGGGCCC CTGATCTGCA ACGGTACTT GCAGGGCCTT      540
GTGTCTTTCG GAAAAGCCCC GTGTGGCCAA CTTGGCGTGC CAGGTGTCTA CACCAACCTC      600
TGCAAATTCA CTGAGTGGAT AGAGAAAACC GTCCAGNCCA GTTAACTCTG GGGACTGGGA      660
ACCCATGAAA TTGACCCCA AATACATCCT GCGGAANGAA TTCAGGAATA TCTGTTCCCA      720
GCCCCTCCTC CCTCAGGCC AGGAGTCCAG GCCCCAGCC CCTCCTCCCT CAAACCAAGG      780
GTACAGATCC CCAGCCCCTC CTCCCTCAGA CCCAGGAGTC CAGACCCCC AGCCCCCTNT      840
CCNTCAGACC CAGGAGTCCA GCCCCTCCTC CNTCAGACGC AGGAGTCCAG ACCCCCAGC      900
CCNTCNTCCG TCAGACCCAG GGGTGCAGGC CCCCACCCCTC TCNTCCNTCA GAGTCAGAGG      960
TCCAAGCCCC CAACCCCTCG TTCCCAGAC CCAGAGGTNC AGGTCCCAGC CCCTCCTCCC      1020
TCAGACCCAG CGGTCCAATG CCACCTAGAN TNTCCCTGTA CACAGTGCCC CCTTGTGGCA      1080
NGTTGACCCA ACCTTACCAG TTGGTTTTTC ATTTTTTTGTC CCTTTCCCCT AGATCCAGAA      1140
ATAAAGTNTA AGAGAAGCGC AAAAAAA

```

(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

```

Met Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln Trp
1           5           10           15
Val Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu
20           25           30
Gly Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val

```

116

35	40	45
Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Leu Leu Leu		
50	55	60
Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser		
65	70	75
Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly		
85	90	95
Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly Arg Met		
100	105	110
Pro Thr Val Leu His Cys Val Asn Val Ser Val Val Ser Glu Xaa Val		
115	120	125
Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe Cys Ala		
130	135	140
Gly Gly Gly Gln Asp Gln Lys Asp Ser Cys Asn Gly Asp Ser Gly Gly		
145	150	155
Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe Gly Lys		
165	170	175
Ala Pro Cys Gly Gln Leu Gly Val Pro Gly Val Tyr Thr Asn Leu Cys		
180	185	190
Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Xaa Ser		
195	200	205

(2) INFORMATION FOR SEQ ID NO:177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1119 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

GCGCACTCGC AGCCCTGGCA GCGGCACTG GTCATGGAAA ACGAATTGTT CTGCTCGGGC	60
GTCCTGGTGC ATCCGCAGTG GGTGCTGTCA GCCGCACACT GTTCCAGAA CTCCTACACC	120
ATCGGGCTGG GCCTGCACAG TCTTGAGGCC GACCAAGAGC CAGGGAGCCA GATGGTGGAG	180
GCCAGCCTCT CCGTACGGCA CCCAGAGTAC AACAGACCCT TGCTCGCTAA CGACCTCATG	240
CTCATCAAGT TGGACGAATC CGTGTCGAG TCTGACACCA TCCGGAGCAT CAGCATTGCT	300
TCGCAGTGCC CTACCGCGGG GAACTCTTGC CTCGTTTCTG GCTGGGGTCT GCTGGCGAAC	360
GATGCTGTGA TTGCCATCCA GTCCCAGACT GTGGGAGGCT GGGAGTGTGA GAAGCTTTCC	420
CAACCCTGGC AGGGTTGTAC CATTCGGCA ACTTCCAGTG CAAGGACGTC CTGCTGCATC	480

```

CTCACTGGGT GCTCACTACT GCTCACTGCA TCACCCGGAA CACTGTGATC AACTAGCCAG      540
CACCATAGTT CTCCGAAGTC AGACTATCAT GATTACTGTG TTGACTGTGC TGTCTATTGT      600
ACTAACCATG CCGATGTTTA GGTGAAATTA GCGTCACTTG GCCTCAACCA TCTTGGTATC      660
CAGTTATCCT CACTGAATTG AGATTTTCCTG CTTCAAGTGC AGCCATTCCC ACATAATTTT      720
TGACCTACAG AGGTGAGGGA TCATATAGCT CTTCAAGGAT GCTGGTACTC CCCTCACAAA      780
TTCATTTTCT CTGTTGTAGT GAAAGGTGCG CCCTCTGGAG CCTCCCAGGG TGGGTGTGCA      840
GGTCACAATG ATGAATGTAT GATCGTGTTC CCATTACCCA AAGCCTTTAA ATCCCTCATG      900
CTCAGTACAC CAGGGCAGGT CTAGCATTTT TTCATTTAGT GTATGCTGTC CATTCATGCA      960
ACCACCTCAG GACTCCTGGA TTCTCTGCCT AGTTGAGCTC CTGCATGCTG CCTCCTTGGG     1020
GAGGTGAGGG AGAGGGCCCA TGGTTCAATG GGATCTGTGC AGTTGTAACA CATTAGGTGC     1080
TTAATAAACA GAAGCTGTGA TGTTAAAAAA AAAAAAAAAA     1119

```

(2) INFORMATION FOR SEQ ID NO:178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

```

Met Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln Trp
 1              5              10              15

Val Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu
 20              25              30

Gly Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val
 35              40              45

Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro Leu Leu
 50              55              60

Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser
 65              70              75              80

Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly
 85              90              95

Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Asp Ala Val
 100             105             110

Ile Ala Ile Gln Ser Xaa Thr Val Gly Gly Trp Glu Cys Glu Lys Leu
 115             120             125

Ser Gln Pro Trp Gln Gly Cys Thr Ile Ser Ala Thr Ser Ser Ala Arg
 130             135             140

Thr Ser Cys Cys Ile Leu Thr Gly Cys Ser Leu Leu Leu Thr Ala Ser

```

145

150

155

160

Pro Gly Thr Leu

(2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

CTGGAGTGCC TTGGTGTTC AAGCCCCTGC AGGAAGCAGA ATGCACCTTC TGAGGCACCT	60
CCAGTGCCC CCGGCCGGG GATGCGAGGC TCGGAGCACC CTTGCCCGGC TGTGATTGCT	120
GCCAGGCACT GTTCATCTCA GCTTTTCTGT CCCTTTGCTC CCGCAAGCG CTTCTGCTGA	180
AAGTTCATAT CTGGAGCCTG ATGTCTTAAC GAATAAAGGT CCCATGCTCC ACCCGAAAAA	240
AAAAAAAAAA	250

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

ACTAGTCCAG TGTGGTGGAA TTCCATTGTG TTGGGCCCAA CACAATGGCT ACCTTTAACA	60
TCACCCAGAC CCCGCCCTG CCCGTGCCCC ACGCTGCTGC TAACGACAGT ATGATGCTTA	120
CTCTGCTACT CGGAACTAT TTTTATGTAA TTAATGTATG CTTTCTTGTT TATAAATGCC	180
TGATTAAAA AAAAAAAAAA AA	202

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 558 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

TCCYTTTGKT NAGGTTTKKG AGACAMCCCK AGACCTWAAN CTGTGTCACA GACTTCYNGG	60
AATGTTTAGG CAGTGCTAGT AATTCYTCG TAATGATTCT GTTATTACTT TCCTNATTCT	120
TTATTCCTCT TTCTTCTGAA GATTAATGAA GTTGAAAATT GAGGTGGATA AATACAAAAA	180
GGTAGTGTGA TAGTATAAGT ATCTAAGTGC AGATGAAAGT GTGTTATATA TATCCATTCA	240
AAATTATGCA AGTTAGTAAT TACTCAGGGT TAACTAAATT ACTTTAATAT GCTGTTGAAC	300
CTACTCTGTT CCTTGGCTAG AAAAAATTAT AAACAGGACT TTGTTAGTTT GGAAGCCAA	360
ATTGATAATA TTCTATGTTT TAAAAGTTGG GCTATACATA AATTATTAAG AAATATGGAW	420

TTTTATTCCC	AGGAATATGG	KGTTCAATTT	ATGAATATTA	CSCRGGATAG	AWGTWTGAGT	480
AAAAYCAGTT	TTGGTWAATA	YGTWAATATG	TCMTAAATAA	ACAAKGCTTT	GACTTATTTT	540
CAAAAAAAAA	AAAAAAAA					558

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

ACAGGGWTTK	GRGGATGCTA	AGSCCCCRGA	RWTYGTTTGA	TCCAACCCTG	GCTTWTTTTC	60
AGAGGGGAAA	ATGGGGCCTA	GAAGTTACAG	MSCATYTAGY	TGGTGCGMTG	GCACCCCTGG	120
CSTCACACAG	ASTCCCGAGT	AGCTGGGACT	ACAGGCACAC	AGTCACTGAA	GCAGGCCCTG	180
TTWGCAATTC	ACGTTGCCAC	CTCCAACCTA	AACATTCTTC	ATATGTGATG	TCCTTAGTCA	240
CTAAGGTTAA	ACTTTCCAC	CCAGAAAAGG	CAACTTAGAT	AAAATCTTAG	AGTACTTTCA	300
TACTMTTCTA	AGTCCTCTTC	CAGCCTCACT	KKGAGTCCTM	CYTGGGGGTT	GATAGGAANT	360
NTCTCTTGGC	TTTCTCAATA	AARTCTCTAT	YCATCTCATG	TTTAATTGG	TACGCATARA	420
AWTGSTGARA	AAATTAATAA	GTTCTGGTTY	MACTTTAAAA	AAAAAAAAAA	AAAAAAAAAA	479

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

AGGCGGGAGC	AGAAGCTAAA	GCCAAAGCCC	AAGAAGAGTG	GCAGTGCCAG	CACTGGTGCC	60
AGTACCAGTA	CCAATAACAG	TGCCAGTGCC	AGTGCCAGCA	CCAGTGGTGG	CTTCAGTGCT	120
GGTGCCAGCC	TGACCGCCAC	TCTCACATTT	GGGCTCTTCG	CTGGCCTTGG	TGGAGCTGGT	180
GCCAGCACCA	GTGGCAGCTC	TGGTGCCTGT	GGTTTCTCCT	ACAAGTGAGA	TTTTAGATAT	240
TGTTAATCCT	GCCAGTCTTT	CTCTTCAAGC	CAGGGTGCAT	CCTCAGAAAC	CTACTCAACA	300
CAGCACTCTA	GGCAGCCACT	ATCAATCAAT	TGAAGTTGAC	ACTCTGCATT	ARATCTATTT	360
GCCATTTCAA	AAAAAAAAAA	AAAA				384

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

ACCGAATTGG	GACCGCTGGC	TTATAAGCGA	TCATGTYTNT	CCRGATKAC	CTCAACGAGC	60
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120

AGGGAGATCG	AGTCTATACG	CTGAAGAAAT	TTGACCCGAT	GGGACAACAG	ACCTGCTCAG	120
CCCATCCTGC	TCGGTTCTCC	CCAGATGACA	AATACTCTSG	ACACCGAATC	ACCATCAAGA	180
AACGCTTCAA	GGTGCTCATG	ACCCAGCAAC	CGCGCCCTGT	CCTCTGAGGG	TCCCTTAAAC	240
TGATGTCTTT	TCTGCCACCT	GTTACCCCTC	GGAGACTCCG	TAACCAAAC	CTTCGGACTG	300
TGAGCCCTGA	TGCCTTTTGT	CCAGCCATAC	TCTTTGGCAT	CCAGTCTCTC	GTGGCGATTG	360
ATTATGCTTG	TGTGAGGCAA	TCATGGTGGC	ATCACCCATA	AAGGGAACAC	ATTTGACTTT	420
TTTTTCTCAT	ATTTTAAAT	ACTACMAGAW	TATTWMAGAW	WAAATGAWTT	GAAAAACTST	480
TAAAAA	AAAAA					496

(2) INFORMATION FOR SEQ ID NO:185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

GCTGGTAGCC	TATGGCGKGG	CCCACGGAGG	GGCTCCTGAG	GCCACGGRAC	AGTGACTTCC	60
CAAGTATCYT	GCGCSGCGTC	TTCTACCGTC	CCTACCTGCA	GATCTTCGGG	CAGATTCCCC	120
AGGAGGACAT	GGACGTGGCC	CTCATGGAGC	ACAGCAACTG	YTCGTGCGAG	CCCGGCTTCT	180
GGGCACACCC	TCCTGGGGCC	CAGGCGGGCA	CCTGCGTCTC	CCAGTATGCC	AÀCTGGCTGG	240
TGGTGCTGCT	CCTCGTCATC	TTCCTGCTCG	TGGCCAACAT	CCTGCTGGTC	AACTTGCTCA	300
TTGCCATGTT	CAGTTACACA	TTCGGCAAAG	TACAGGGCAA	CAGCGATCTC	TACTGGGAAG	360
GCGCAGCGTT	ACCGCCTCAT	CCGG				384

(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 577 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

GAGTTAGCTC	CTCCACAACC	TTGATGAGGT	CGTCTGCAGT	GGCCTCTCGC	TTCATACCGC	60
TNCCATCGTC	ATACTGTAGG	TTTGCCACCA	CYTCTGGCA	TCTTGGGGCG	GCNTAATATT	120
CCAGGAAACT	CTCAATCAAG	TCACCGTCGA	TGAAACCTGT	GGGCTGGTTC	TGTCTTCCGC	180
TCGGTGTGAA	AGGATCTCCC	AGAAGGAGTG	CTCGATCTTC	CCCACACTTT	TGATGACTTT	240
ATTGAGTCGA	TTCTGCATGT	CCAGCAGGAG	GTTGTACCAG	CTCTCTGACA	GTGAGGTCAC	300
CAGCCCTATC	ATGCCGTTGA	MCGTGCCGAA	GARCACCGAG	CCTTGTGTGG	GGGKKGAAGT	360
CTCACCCAGA	TTCTGCATTA	CCAGAGAGCC	GTGGCAAAAG	ACATTGACAA	ACTCGCCCAG	420
GTGGA AAAAAG	AMCAMCTCCT	GGARGTGCTN	GCCGCTCCTC	GTCMGTGGT	GGCAGCGCTW	480
TCCTTTTGAC	ACACAAACAA	GTTAAAGGCA	TTTTAGCC	CCAGAAANTT	GTCATCATCC	540
AAGATNTCGC	ACAGCACTNA	TCCAGTTGGG	ATTAAAT			577

(2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 534 base pairs
- (B) TYPE: nucleic acid

121

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

AACATCTTCC	TGTATAATGC	TGTGTAATAT	CGATCCGATN	TTGTCTGSTG	AGAATYCATW	60
ACTKGGAAAA	GMAACATTAA	AGCCTGGACA	CTGGTATTAA	AATTCACAAT	ATGCAACACT	120
TTAAACAGTG	TGTCAATCTG	CTCCCYYNAC	TTTGTTCATCA	CCAGTCTGGG	AKAAGGGTA	180
TGCCCTATTC	ACACCTGTTA	AAAGGGCGCT	AAGCATTTTT	GATTCAACAT	CTTTTTTTTT	240
GACACAAGTC	CGAAAAAAGC	AAAAGTAAAC	AGTTATYAAT	TTGTTAGCCA	ATTCACCTTC	300
TTCATGGGAC	AGAGCCATYT	GATTTAAAAA	GCAAATTGCA	TAATATTGAG	CTTYGGGAGC	360
TGATATTGGA	GCGGAAGAGT	AGCCTTCTTA	CTTCACCAGA	CACAACTCCC	TTTCATATTG	420
GGATGTTNAC	NAAAGTWATG	TCTCTWACAG	ATGGGATGCT	TTTGTGGCAA	TTCTGTTCTG	480
AGGATCTCCC	AGTTTATTTA	CCACTTGCAC	AAGAAGGCGT	TTTCTTCCTC	AGGC	534

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 761 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

AGAAACCAGT	ATCTCTNAAA	ACAACCTCTC	ATACCTTGTG	GACCTAATTT	TGTGTGCGTG	60
TGTGTGTGCG	CGCATATTAT	ATAGACAGGC	ACATCTTTTT	TACTTTTGTA	AAAGCTTATG	120
CCTCTTTGGT	ATCTATATCT	GTGAAAGTTT	TAATGATCTG	CCATAATGTC	TTGGGGACCT	180
TTGTCTTCTG	TGTAAATGGT	ACTAGAGAAA	ACACCTATNT	TATGAGTCAA	TCTAGTTNGT	240
TTTATTCGAC	ATGAAGGAAA	TTTCCAGATN	ACAACACTNA	CAAACCTCTC	CTKGACKARG	300
GGGGACAAAG	AAAAGCAAAA	CTGAMCATAA	RAAACAATWA	CCTGGTGAGA	ARTTGCATAA	360
ACAGAAATWR	GGTAGTATAT	TGAARNACAG	CATCATTAAT	RMGTTWTKTT	WTTCTCCCTT	420
GCAAAAAACA	TGTACNGACT	TCCCGTTGAG	TAATGCCAAG	TTGTTTTTTT	TATNATAAAA	480
CTTGCCCTTC	ATTACATGTT	TNAAAGTGGT	GTGGTGGGCC	AAAATATTGA	AATGATGGAA	540
CTGACTGATA	AAGCTGTACA	AATAAGCAGT	GTGCCTAACA	AGCAACACAG	TAATGTTGAC	600
ATGCTTAATT	CACAAATGCT	AATTTCATTA	TAAATGTTTT	CTAAAATACA	CTTTGAACATA	660
TTTTTCTGTN	TTCCAGAGC	TGAGATNTTA	GATTTTATGT	AGTATNAAGT	GAAAAANTAC	720
GAAATAATA	ACATTGAAGA	AAAANANAAA	AAANAAAAAA	A		761

(2) INFORMATION FOR SEQ ID NO:189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

TTTTTTTTTT	TTTGCCGATN	CTACTATTTT	ATTGCAGGAN	GTGGGGGTGT	ATGCACCGCA	60
CACCGGGGCT	ATNAGAAGCA	AGAAGGAAGG	AGGGAGGGCA	CAGCCCCTTG	CTGAGCAACA	120
AAGCCGCCTG	CTGCCTTCTC	TGTCTGTCTC	CTGGTGCAGG	CACATGGGGA	GACCTTCCCC	180

AAGGCAGGGG	CCACCAGTCC	AGGGGTGGGA	ATACAGGGGG	TGGGANGTGT	GCATAAGAAG	240
TGATAGGCAC	AGGCCACCCG	GTACAGACCC	CTCGGCTCCT	GACAGGTNGA	TTTCGACCAG	300
GTCATTGTGC	CCTGCCCAGG	CACAGCGTAN	ATCTGGAAAA	GACAGAATGC	TTTCCTTTTC	360
AAATTTGGCT	NGTCATNGAA	NGGGCANTTT	TCCAANTTNG	GCTNGGTCTT	GGTACNCTTG	420
GTTCGGCCCA	GCTCCNCGTC	CAAAAANTAT	TCACCCNNCT	CCNAATTGCT	TGCNGGNCCC	480
CC						482

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

TTTTTTTTTT	TTTTAAACA	GTTTTTCACA	ACAAAATTTA	TTAGAAGAAT	AGTGGTTTTG	60
AAAACCTCTG	CATCCAGTGA	GAAC TACCAT	ACACCACATT	ACAGCTNGGA	ATGTNCTCCA	120
AATGTCTGGT	CAAATGATAC	AATGGAACCA	TTCAATCTTA	CACATGCACG	AAAGAACAAG	180
CGCTTTTGAC	ATACAATGCA	CAAAAAAAAA	AGGGGGGGGG	GACCACATGG	ATTAAAATTT	240
TAAGTACTCA	TCACATACAT	TAAGACACAG	TTCTAGTCCA	GTCTNAAAATC	AGAACTGCNT	300
TGAAAAATTT	CATGTATGCA	ATCCAACCAA	AGAACTTNAT	TGGTGATCAT	GANTNCTCTA	360
CTACATCNAC	CTTGATCATT	GCCAGGAACN	AAAAGTTNAA	ANCACNCNGT	ACAAAAANAA	420
TCTGTAATTN	ANTTCAACCT	CCGTACNGAA	AAATNTTNTT	TATACACTCC	C	471

(2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

GAGGGATTGA	AGGTCTGTTC	TASTGTCGGM	CTGTTCAGCC	ACCAACTCTA	ACAAGTTGCT	60
GTCTTCCACT	CACTGTCTGT	AAGCTTTTTA	ACCCAGACWG	TATCTTCATA	AATAGAACAA	120
ATTCTTCACC	AGTCACATCT	TCTAGGACCT	TTTTGGATTC	AGTTAGTATA	AGCTCTTCCA	180
CTTCCTTTGT	TAAGACTTCA	TCTGGTAAAG	TCCTAAGTTT	TGTAGAAAGG	AATTYAATTG	240
CTCGTTCTCT	AACAATGTCC	TCTCCTTGAA	GTATTTGGCT	GAACAACCCA	CCTAAAGTCC	300
CTTTGTGCAT	CCATTTTAAA	TATACTTAAT	AGGGCATTGK	TNCACTAGGT	TAAATTCTGC	360
AAGAGTCATC	TGTCTGCAAA	AGTTGCGTTA	GTATATCTGC	CA		402

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

GAGCTCGGAT	CCAATAATCT	TTGTCTGAGG	GCAGCACACA	TATNCAGTGC	CATGGNAACT	60
GGTCTACCCC	ACATGGGAGC	AGCATGCCGT	AGNTATATAA	GGTCATTCCC	TGAGTCAGAC	120
ATGCTYTYTT	GAYTACCGTG	TGCCAAGTGC	TGGTGATTCT	YAACACACYT	CCATCCCGYT	180
CTTTTGTGGA	AAAACCTGGCA	CTTKTCTGGA	ACTAGCARGA	CATCACTTAC	AAATTACCCC	240
ACGAGACACT	TGAAAGGTGT	AACAAAGCGA	YTCTTGCAAT	GCTTTTTGTC	CCTCCGGCAC	300
CAGTTGTCAA	TACTAACCCG	CTGGTTTGCC	TCCATCACAT	TTGTGATCTG	TAGCTCTGGA	360
TACATCTCCT	GACAGTACTG	AAGAACTTCT	TCTTTTGTGT	CAAAAGCARG	TCTTGGTGCC	420
TGTTGGATCA	GGTTCCCAT	TCCCAGTCYG	AATGTTTACA	TGGCATATTT	WACTTCCCAC	480
AAAACATTGC	GATTTGAGGC	TCAGCAACAG	CAAATCCTGT	TCCGGCATTG	GCTGCAAGAG	540
CCTCGATGTA	GCCGGCCAGC	GCCAAGGCAG	GCGCCGTGAG	CCCCACCAGC	AGCAGAAGCA	600
G						601

(2) INFORMATION FOR SEQ ID NO:193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 608 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

ATACAGCCCA	NATCCCACCA	CGAAGATGCG	CTTGTTGACT	GAGAACCTGA	TGCGGTCACT	60
GGTCCCGCTG	TAGCCCCAGC	GACTCTCCAC	CTGCTGGAAG	CGGTTGATGC	TGCACTCYTT	120
CCCAACGCAG	GCAGMAGCGG	GSCCGGTCAA	TGAACTCCAY	TCGTGGCTTG	GGGTGACGG	180
TKAAGTGCAG	GAAGAGGCTG	ACCACCTCGC	GGTCCACCAG	GATGCCCCGAC	TGTGCGGGAC	240
CTGCAGCGAA	ACTCCTCGAT	GGTCATGAGC	GGGAAGCGAA	TGAGGCCAG	GGCCTTGCCC	300
AGAACCTTCC	GCCTGTTCTC	TGGCGTCACC	TGCAGCTGCT	GCCGCTGACA	CTCGGCCTCG	360
GACCAGCGGA	CAAACGGCRT	TGAACAGCCG	CACCTCACGG	ATGCCCAGTG	TGTCGCGCTC	420
CAGGAMMGS	ACCAGCGTGT	CCAGGTCAAT	GTCGGTGAAG	CCCTCCGCGG	GTRATGGCGT	480
CTGCAGTGTT	TTTGTGATG	TTCTCCAGGC	ACAGGCTGGC	CAGCTGCGGT	TCATCGAAGA	540
GTCGCGCCTG	CGTGAGCAGC	ATGAAGGCGT	TGTCGGCTCG	CAGTTCTTCT	TCAGGAACTC	600
CACGCAAT						608

(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

GAACGGCTGG	ACCTTGCCCTC	GCATTGTGCT	TGCTGGCAGG	GAATACCTTG	GCAAGCAGYT	60
CCAGTCCGAG	CAGCCCCAGA	CCGCTGCCGC	CCGAAGCTAA	GCCTGCCTCT	GGCCTTCCCC	120
TCCGCTCAA	TGCAGAACCA	GTAGTGGGAG	CAGTGTGTTT	AGAGTTAAGA	GTGAACACTG	180
TTTGATTTTA	CTTGGAATT	TCCTCTGTTA	TATAGCTTTT	CCCAATGCTA	ATTTCCAAAC	240
AACAACAACA	AAATAACATG	TTTGCCTGTT	AAGTTGTATA	AAAGTAGGTG	ATTCTGTATT	300
TAAAGAAAAT	ATTACTGTTA	CATATACTGC	TTGCAATTTT	TGTATTTATT	GKTNCTSTGG	360
AAATAAATAT	AGTTATTAAA	GGTTGTCANT	CC			392

(2) INFORMATION FOR SEQ ID NO:195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

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CCSTTKGAGG GGTKAGGKYC CAGTTYCCGA GTGGAAGAAA CAGGCCAGGA GAAGTGCCTG      60
CCGAGCTGAG GCAGATGTTC CCACAGTGAC CCCCAGAGCC STGGGSTATA GTYTCTGACC      120
CCTCNCAAGG AAAGACCACS TTCTGGGGAC ATGGGCTGGA GGCAGGACC TAGAGGCACC      180
AAGGGAAGGC CCCATTCCGG GGSTGTTCCC CGAGGAGGAA GGAAGGGGC TCTGTGTGCC      240
CCCCASGAGG AAGAGGCCCT GAGTCCTGGG ATCAGACACC CCTTCACGTG TATCCCCACA      300
CAAATGCAAG CTCACCAAGG TCCCCTCTCA GTCCCTTCC STACACCCTG AMCGGCCACT      360
GSCSCACACC CACCCAGAGC ACGCCACCCG CCATGGGGAR TGTGCTCAAG GARTCGCNGG      420
GCARCGTGGA CATCTNGTCC CAGAAGGGGG CAGAATCTCC AATAGANGGA CTGARCMSTT      480
GCTNANAAAA AAAANAAAA AA                                     502

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(2) INFORMATION FOR SEQ ID NO:196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 665 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

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GGTTACTTGG TTTCATTGCC ACCACTTAGT GGATGTCATT TAGAACCATT TTGTCTGCTC      60
CCTCTGGAAG CCTTGCGCAG AGCGGACTTT GTAATTGTTG GAGAATAACT GCTGAATTTT      120
WAGCTGTTTK GAGTTGATTS GCACCACTGC ACCCACAAC TCAATATGAA AACYAWTTGA      180
ACTWATTTAT TATCTTGTGA AAAGTATAAC AATGAAAATT TTGTTTATAC TGTATTKATC      240
AAGTATGATG AAAAGCAAWA GATATATATT CTTTTATTAT GTTAAATTAT GATTGCCATT      300
ATTAATCGGC AAAATGTGGA GTGTATGTTT TTTTCACAGT AATATATGCC TTTTGTAAC T      360
TCACTTGGTT ATTTTATTGT AAATGARTTA CAAAATTCTT AATTTAAGAR AATGGTATGT      420
WATATTTATT TCATTAATTT CTTTCCTKGT TTACGTWAAT TTTGAAAAGA WTGCATGATT      480
TCTTGACAGA AATCGATCTT GATGCTGTGG AAGTAGTTTG ACCCACATCC CTATGAGTTT      540
TTCTTAGAAT GTATAAAGGT TGTAGCCCAT CNAACTTCAA AGAAAAAAT GACCACATAC      600
TTTGCAATCA GGCTGAAATG TGGCATGCTN TTCTAATTCC AACTTTATAA ACTAGCAAAN      660
AAGT

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(2) INFORMATION FOR SEQ ID NO:197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 492 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

TTTTNTTTTT	TTTTTTTTGC	AGGAAGGATT	CCATTTATTG	TGGATGCATT	TTCACAATAT	60
ATGTTTATTG	GAGCGATCCA	TTATCAGTGA	AAAGTATCAA	GTGTTTATAA	NATTTTTAGG	120
AAGGCAGATT	CACAGAACAT	GCTNGTCNGC	TTGCAGTTTT	ACCTCGTANA	GATNACAGAG	180
AATTATAGTC	NAACCAGTAA	ACNAGGAATT	TACTTTTCAA	AAGATTAAAT	CCTAACTGAA	240
CAAAATTCTA	CCCTGAAACT	TACTCCATCC	AAATATTGGA	ATAANAGTCA	GCAGTGATAC	300
ATTCTCTTCT	GAACTTTAGA	TTTTCTAGAA	AAATATGTAA	TAGTGATCAG	GAAGAGCTCT	360
TGTTCAAAAG	TACAACNAAG	CAATGTTCCC	TTACCATAGG	CCTTAATTCA	AACTTTGATC	420
CATTTCACTC	CCATCACGGG	AGTCAATGCT	ACCTGGGACA	CTTGTATTTT	GTTCATNCTG	480
ANCNTGGCTT	AA					492

(2) INFORMATION FOR SEQ ID NO:198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

TTTNTTTTGN	ATTTTCANTCT	GTANNAANTA	TTTTCATTAT	GTTTATTANA	AAAATATNAA	60
TGTNTCCACN	ACAAATCATN	TTACNTNAGT	AAGAGGCCAN	CTACATTGTA	CAACATACAC	120
TGAGTATATT	TTGAAAAGGA	CAAGTTTAAA	GTANACNCAT	ATTGCCGANC	ATANCACATT	180
TATACATGGC	TTGATTGATA	TTAGCACAG	CANAACTGA	GTGAGTTACC	AGAAANAAAT	240
NATATATGTC	AATCNGATTT	AAGATACAAA	ACAGATCCTA	TGGTACATAN	CATCNTGTAG	300
GAGTTGTGGC	TTTATGTTTA	CTGAAAGTCA	ATGCAGTTCC	TGTACAAAGA	GATGGCCGTA	360
AGCATTCTAG	TACCTCTACT	CCATGGTTAA	GAATCGTACA	CTTATGTTTA	CATATGTNCA	420
GGGTAAGAAT	TGTGTTAAGT	NAANTTATGG	AGAGGTCCAN	GAGAAAAATT	TGATNCAA	478

(2) INFORMATION FOR SEQ ID NO:199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

AGTGACTTGT	CCTCCAACAA	AACCCCTTGA	TCAAGTTTGT	GGCACTGACA	ATCAGACCTA	60
TGCTAGTTCC	TGTCATCTAT	TCGCTACTAA	ATGCAGACTG	GAGGGGACCA	AAAAGGGGCA	120
TCAACTCCAG	CTGGATTATT	TTGGAGCCTG	CAAATCTATT	CCTACTTGTA	CGGACTTTGA	180
AGTGATTGAG	TTTCCTCTAC	GGATGAGAGA	CTGGCTCAAG	AATATCCTCA	TGCAGCTTTA	240
TGAAGCCNAC	TCTGAACACG	CTGGTTATCT	NAGATGAGAA	NCAGAGAAAT	AAAGTCNAGA	300
AAATTTACCT	GGANGAAAAG	AGGCTTTNGG	CTGGGGACCA	TCCCATTGAA	CCTTCTCTTA	360
ANGGACTTTA	AGAANAAACT	ACCACATGTN	TGTNGTATCC	TGGTGCCNGG	CCGTTTANTG	420
AACNTNGACN	NCACCCTTNT	GGAATANANT	CTTGACNGCN	TCCTGAACTT	GCTCCTCTGC	480
GA						482

(2) INFORMATION FOR SEQ ID NO:200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

CGGCCGCAAG TGCAACTCCA GCTGGGGCCG TGCGGACGAA GATTCTGCCA GCAGTTGGTC	60
CGACTGCGAC GACGGCGGCG GCGACAGTCG CAGGTGCAGC GCGGGCGCCT GGGGTCTTGC	120
AAGGCTGAGC TGACGCCGCA GAGGTCGTGT CACGTCCCAC GACCTTGACG CCGTCGGGGA	180
CAGCCGGAAC AGAGCCCGGT GAANGCGGGA GGCCTCGGGG AGCCCCTCGG GAAGGGCGGC	240
CCGAGAGATA CGCAGGTGCA GGTGGCCGCC	270

(2) INFORMATION FOR SEQ ID NO:201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 419 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

TTTTTTTTTT TTTTGAATC TACTGCGAGC ACAGCAGGTC AGCAACAAGT TTATTTTGCA	60
GCTAGCAAGG TAACAGGGTA GGGCATGGTT ACATGTTTCAG GTCAACTTCC TTGTCTGTGG	120
TTGATTGGTT TGTCTTTATG GGGGCGGGGT GGGGTAGGGG AAANCGAAGC ANAANTAACA	180
TGGAGTGGGT GCACCTCCC TGTAGAACCT GGTACNAAA GCTTGGGGCA GTTCACCTGG	240
TCTGTGACCG TCATTTTCTT GACATCAATG TTATTAGAAG TCAGGATATC TTTTAGAGAG	300
TCCACTGTNT CTGGAGGGAG ATTAGGGTTT CTTGCCAANA TCCAANCAAA ATCCACNTGA	360
AAAAGTTGGA TGATNCANGT ACNGAATACC GANGGCATAN TTCTCATANT CGGTGGCCA	419

(2) INFORMATION FOR SEQ ID NO:202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

TTTNTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT	60
TGGCACTTAA TCCATTTTAA TTTCAAAATG TCTACAAANT TTNAATNCNC CATTATACNG	120
GTNATTTTNC AAAATCTAAA NNTTATTCAA ATNTNAGCCA AANTCCTTAC NCAAAATNNAA	180
TACNCNCAAA AATCAAAAAT ATACNTNTCT TTCAGCAAAC TTNGTTACAT AAATTAAAAA	240
AATATATACG GCTGGTGTTT TCAAAGTACA ATTATCTTAA CACTGCAAAC ATNTTTNNAA	300
GGAACATAAA TAAAAAATAA CACTNCCGCA AAGGTTAAAG GGAACAACAA ATTCNTTTTA	360
CAACANCNNC NATTATAAAA ATCATATCTC AAATCTTAGG GGAATATATA CTTACACNG	420
GGATCTTAAC TTTTACTNCA CTTTGTATAT TTTTTTANAA CCATTGTNTT GGGCCCAACA	480
CAATGGNAAT NCCNCCNCNC TGGACTAGT	509

(2) INFORMATION FOR SEQ ID NO:203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 583 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

```

TTTTTTTTTT TTTTTTTTGA CCCCCCTCTT ATAAAAACA AGTTACCATT TTATTTTACT      60
TACACATATT TATTTTATAA TTGGTATTAG ATATTCAAAA GGCAGCTTTT AAAATCAAAC      120
TAAATGGAAA CTGCCTTAGA TACATAATTC TTAGGAATTA GCTTAAATC TGCCTAAAGT      180
GAAAATCTTC TCTAGCTCTT TTGACTGTAA ATTTTGGACT CTTGTAAAAC ATCCAAATTC      240
ATTTTCTCTG CCTTTAAAT TATCTAATCT TTCCATTTT TCCCTATTCC AAGTCAATTT      300
GCTTCTCTAG CCTCATTTC TAGCTCTTAT CTACTATTAG TAAGTGGCTT TTTTCCTAAA      360
AGGGAAAACA GGAAGAGANA ATGGCACACA AAACAAACAT TTTATATTCA TATTTCTACC      420
TACGTTAATA AAATAGCATT TTGTGAAGCC AGCTCAAAAG AAGGCTTAGA TCCTTTTATG      480
TCCATTTTAG TCACTAAACG ATATCNAAAG TGCCAGAATG CAAAAGGTTT GTGAACATTT      540
ATTCAAAAGC TAATATAAGA TATTTACAT ACTCATCTT CTG                               583

```

(2) INFORMATION FOR SEQ ID NO:204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 589 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

```

TTTTTTTTNT TTTTTTTTTT TTTTNTCTC TTCTTTTTTT TTGANAATGA GGATCGAGTT      60
TTTCACTCTC TAGATAGGGC ATGAAGAAAA CTCATCTTTC CAGCTTTAAA ATAACAATCA      120
AATCTCTTAT GCTATATCAT ATTTTAAGTT AACTAATGA GTCACTGGCT TATCTTCTCC      180
TGAAGGAAAT CTGTTCAATC TTCTCATTCA TATAGTTATA TCAAGTACTA CCTTGCATAT      240
TGAGAGGTTT TTCTTCTCTA TTTACACATA TATTCCATG TGAATTTGTA TCAAACCTTT      300
ATTTTCATGC AACTAGAAA ATAATGTNTT CTTTGCATA AGAGAAGAGA ACAATATNAG      360
CATTACAAA CTGCTCAAAT TGTTGTAA GNTTATCCAT TATAATTAGT TNGGCAGGAG      420
CTAATACAAA TCACATTTAC NGACNAGCAA TAATAAACT GAAGTACCAG TTAAATATCC      480
AAAATAATTA AAGGAACATT TTTAGCCTGG GTATAATTAG CTAATTCAT TTACAAGCAT      540
TTATTNAGAA TGAATTCACA TGTTATTATT CCNTAGCCCA ACACAATGG                               589

```

(2) INFORMATION FOR SEQ ID NO:205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 545 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

128

TTTTNTTTT	TTTTTCAGT	AATAATCAGA	ACAATATTTA	TTTTATATT	TAAAATTCAT	60
AGAAAAGTGC	CTTACATTTA	ATAAAAGTTT	GTTTCTCAA	GTGATCAGAG	GAATTAGATA	120
TNGTCTTGAA	CACCAATATT	AATTTGAGGA	AAATACACCA	AAATACATTA	AGTAAATTAT	180
TTAAGATCAT	AGAGCTTGTA	AGTGAAAAGA	TAAAATTTGA	CCTCAGAAAC	TCTGAGCATT	240
AAAAATCCAC	TATTAGCAAA	TAAATTACTA	TGGACTTCTT	GCTTTAATTT	TGTGATGAAT	300
ATGGGGTGTC	ACTGGTAAAC	CAACACATTC	TGAAGGATAC	ATTACTTAGT	GATAGATTCT	360
TATGTACTTT	GCTANATNAC	GTGGATATGA	GTTGACAAGT	TTCTCTTTCT	TCAATCTTTT	420
AAGGGGCNGA	NGAAATGAGG	AAGAAAAGAA	AAGGATTACG	CATACTGTTC	TTTCTATNGG	480
AAGGATTAGA	TATGTTTCCT	TTGCCAATAT	TAAAAAATA	ATAATGTTTA	CTACTAGTGA	540
AACCC						545

(2) INFORMATION FOR SEQ ID NO:206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

TTTTTTTTTT	TTTTTAGTC	AAGTTTCTNA	TTTTTATTAT	AATTAAAGTC	TTGGTCATTT	60
CATTTATTAG	CTCTGCAACT	TACATATTTA	AATTAAAGAA	ACGTTNTTAG	ACAACTGTNA	120
CAATTTATAA	ATGTAAGGTG	CCATTATTGA	GTANATATAT	TCCTCCAAGA	GTGGATGTGT	180
CCCTTCTCCC	ACCAACTAAT	GAANCAGCAA	CATTAGTTTA	ATTTTATTAG	TAGATNATAC	240
ACTGCTGCAA	ACGCTAATTC	TCTTCTCCAT	CCCATGTING	ATATTGTGTA	TATGTGTGAG	300
TTGGTNAGAA	TGCATCANCA	ATCTNACAAT	CAACAGCAAG	ATGAAGCTAG	GCNTGGGCTT	360
TCGGTGAAAA	TAGACTGTGT	CTGTCTGAAT	CAAATGATCT	GACCTATCCT	CGGTGGCAAG	420
AACTCTTCGA	ACCGCTTCCT	CAAAGGCNGC	TGCCACATTT	GTGGCNTCTN	TTGCACTTGT	480
TTCAAAA						487

(2) INFORMATION FOR SEQ ID NO:207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

TGAATTGGCT	AAAAGACTGC	ATTTTTANAA	CTAGCAACTC	TTATTCTTTT	CCTTTAAAAA	60
TACATAGCAT	TAAATCCCAA	ATCCTATTTA	AAGACCTGAC	AGCTTGAGAA	GGTCACTACT	120
GCATTTATAG	GACCTTCTGG	TGGTTCTGCT	GTTACNTTTG	AANTCTGACA	ATCCTTGANA	180
ATCTTTGCAT	GCAGAGGAGG	TAAAAGGTAT	TGGATTTTCA	CAGAGGAANA	ACACAGCGCA	240
GAAATGAAGG	GGCCAGGCTT	ACTGAGCTTG	TCCACTGGAG	GGCTCATGGG	TGGGACATGG	300
AAAAGAAGGC	AGCCTAGGCC	CTGGGGAGCC	CA			332

(2) INFORMATION FOR SEQ ID NO:208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 524 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

```

AGGGCGTGGT GCGGAGGGCG TTACTGTTTT GTCTCAGTAA CAATAAATAC AAAAAGACTG      60
GTTGTGTTCC GGCCCATCC AACCACGAAG TTGATTTCTC TTGTGTGCAG AGTGACTGAT      120
TTTAAAGGAC ATGGAGCTTG TCACAATGTC ACAATGTCAC AGTGTGAAGG GCACACTCAC      180
TCCGCGTGA TTCACATTTA GCAACCAACA ATAGCTCATG AGTCCATACT TGTAAATACT      240
TTTGCCAGAA TACTTNTTGA AACTTGCAGA TGATAACTAA GATCCAAGAT ATTCCCAAA      300
GTAAATAGAA GTGGGTCATA ATATTAATTA CCTGTTTACA TCAGCTTCCA TTTACAAGTC      360
ATGAGCCCGAG AACTGACAT CAACTAAGC CCACTTAGAC TCCTCACCAC CAGTCTGTCC      420
TGTCATCAGA CAGGAGGCTG TCACCTTGAC CAAATTCTCA CCAGTCAATC ATCTATCCAA      480
AAACCATTAC CTGATCCACT TCCGGTAATG CACCACCTTG GTGA                        524

```

(2) INFORMATION FOR SEQ ID NO:209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

```

GGGTGAGGAA ATCCAGAGTT GCCATGGAGA AAATTCCAGT GTCAGCATTC TTGCTCCTTG      60
TGGCCCTCTC CTACACTCTG GCCAGAGATA CCACAGTCAA ACCTGGAGCC AAAAAGGACA      120
CAAAGGACTC TCGACCCAAA CTGCCCCAGA CCCTCTCCA                        159

```

(2) INFORMATION FOR SEQ ID NO:210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

```

ACTCCCTGGC AGACAAAGGC AGAGGAGAGA GCTCTGTTAG TTCTGTGTTG TTGAACTGCC      60
ACTGAATTC TTTCCACTTG GACTATTACA TGCCANTTGA GGGACTAATG GAAAAACGTA      120
TGGGGAGATT TTANCCAATT TANGTNTGTA AATGGGGAGA CTGGGGCAGG CGGGAGAGAT      180
TTGCAGGGTG NAAATGGGAN GGCTGGTTTG TTANATGAAC AGGGACATAG GAGGTAGGCA      240
CCAGGATGCT AAATCA                        256

```

(2) INFORMATION FOR SEQ ID NO:211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

```

ACATTGTTTT TTTGAGATAA AGCATTGAGA GAGCTCTCCT TAACGTGACA CAATGGAAGG      60
ACTGGAACAC ATACCCACAT CTTTGTTCTG AGGGATAATT TTCTGATAAA GTCTTGCTGT      120
ATATTCAAGC ACATATGTTA TATATTATTC AGTTCCATGT TTATAGCCTA GTTAAGGAGA      180
GGGGAGATAC ATTCNGAAAG AGGACTGAAA GAAATACTCA AGTNGGAAAA CAGAAAAAGA      240
AAAAAAGGAG CAAATGAGAA GCCT                                     264

```

(2) INFORMATION FOR SEQ ID NO:212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

```

ACCCAAAAAT CCAATGCTGA ATATTTGGCT TCATTATTCC CANATTCTTT GATTGTCAAA      60
GGATTTAATG TTGTCTCAGC TTGGGCACTT CAGTTAGGAC CTAAGGATGC CAGCCGGCAG      120
GTTTATATAT GCAGCAACAA TATTCAAGCG CGACAACAGG TTATTGAACT TGCCCCCCAG      180
TTNAATTTCA TTCCCATGTA CTTGGGATCC TTATCATCAG CCAGAGAGAT TGAAAATTTA      240
CCCCTACNAC TCTTTACTCT CTGGANAGGG CCAGTGGTGG TAGCTATAAG CTTGGCCACA      300
TTTTTTTTTC CTTTATTCCT TTGTCAGA                                     328

```

(2) INFORMATION FOR SEQ ID NO:213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

```

ACTTATGAGC AGAGCGACAT ATCCNAGTGT AGACTGAATA AACTGAATT CTCTCCAGTT      60
TAAAGCATTG CTCACTGAAG GGATAGAAGT GACTGCCAGG AGGGAAAGTA AGCCAAGGCT      120
CATTATGCCA AAGGANATAT ACATTTCAAT TCTCCAACT TCTTCCTCAT TCCAAGAGTT      180
TTCAATATTT GCATGAACCT GCTGATAANC CATGTTAANA AACAAATATC TCTCTNACCT      240
TCTCATCGGT                                     250

```

(2) INFORMATION FOR SEQ ID NO:214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

```

ACCCAGAATC CAATGCTGAA TATTTGGCTT CATTATTCCC AGATTCTTTG ATTGTCAAAG      60
GATTTAATGT TGTCTCAGCT TGGGCACTTC AGTTAGGACC TAAGGATGCC AGCCGGCAGG      120
TTTATATATG CAGCAACAAT ATTCAAGCGC GACAACAGGT TATTGAACTT GCCCGCCAGT      180
TGAATTTTCA TCCCATTTGAC TTGGGATCCT TATCATCAGC CANAGAGATT GAAAATTTAC      240
CCCTACGACT CTTTACTCTC TGGAGAGGGC CAGTGGTGGT AGCTATAAGC TTGGCCACAT      300
TTTTTTTTC TTTATTCCTT TGTCAGAGAT GCGATTCATC CATATGCTAN AAACCAACAG      360
AGTGACTTTT AAAAAATTCC TATAGANATT GTGAATAAAA CCTTACCTAT AGTTGCCATT      420
ACTTTGCTCT CCCTAATATA CCTC                                     444

```

(2) INFORMATION FOR SEQ ID NO:215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

```

ACTTATGAGC AGAGCGACAT ATCCAAGTGT ANACTGAATA AACTGAATT CTCTCCAGTT      60
TAAAGCATTG CTCACTGAAG GGATAGAAGT GACTGCCAGG AGGGAAAGTA AGCCAAGGCT      120
CATTATGCCA AAGGANATAT ACATTTCAAT TCTCCAACT TCTTCCTCAT TCCAAGAGTT      180
TTCAATATTT GCATGAACCT GCTGATAAGC CATGTTGAGA AACAAATATC TCTCTGACCT      240
TCTCATCGGT AAGCAGAGGC TGTAGGCAAC ATGGACCATA GCGAANAAAA AACTTAGTAA      300
TCCAAGCTGT TTTCTACACT GTAACCAGGT TTCCAACCA GGTGGAAATC TCCTATACTT      360
GGTGCC                                     366

```

(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

```

CTGTATAAAC AGAACTCCAC TGCANGAGGG AGGGCCGGGC CAGGAGAATC TCCGCTTGTC      60
CAAGACAGGG GCCTAAGGAG GGTCTCCACA CTGCTNNTAA GGGCTNTTNC ATTTTTTTAT      120
TAATAAAAAG TNNAAGAGGC CTCTTCTCAA CTTTTTTCCC TTNGGCTGGA AAATTTAAAA      180
ATCAAAAATT TCCTNAAGTT NTCAAGCTAT CATATATACT NTATCCTGAA AAAGCAACAT      240

```

AATTCTTCCT TCCCTCCTTT

260

(2) INFORMATION FOR SEQ ID NO:217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

ACCTACGTGG GTAAGTTTAN AAATGTTATA ATTTTCAGGAA NAGGAACGCA TATAATTGTA	60
TCTTGCCTAT AATTTTCTAT TTAATAAAGG AAATAGCAAA TTGGGGTGGG GCGAATGTAG	120
GGCATTCTAC AGTTTGAGCA AAATGCAATT AAATGTGGAA GGACAGCACT GAAAAATTTT	180
ATGAATAATC TGTATGATTA TATGTCTCTA GAGTAGATTT ATAATTAGCC ACTTACCCTA	240
ATATCCTTCA TGCTTGTAAG GT	262

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

ACCAAGGTGG TGCATTACCG GAANTGGATC AANGACACCA TCGTGGCCAA CCCCTGAGCA	60
CCCCTATCAA CTCCTTTTGG TAGTAAACTT GGAACCTTGG AAATGACCAG GCCAAGACTC	120
AGGCCTCCCC AGTTCTACTG ACCTTTGTCC TTANGTNTNA NGTCCAGGGT TGCTAGGAAA	180
ANAAATCAGC AGACACAGGT GTAAA	205

(2) INFORMATION FOR SEQ ID NO:219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

TACTGTTTTG TCTCAGTAAC AATAAATACA AAAAGACTGG TTGTGTTCCG GCCCCATCCA	60
ACCACGAAGT TGATTCTCT TGTGTGCAGA GTGACTGATT TTAAAGGACA TGGA	114

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:

133

- (A) LENGTH: 93 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

ACTAGCCAGC ACAAAGGCA GGGTAGCCTG AATTGCTTTC TGCTCTTTAC ATTTCTTTTA	60
AAATAAGCAT TTAGTGCTCA GTCCCTACTG AGT	93

(2) INFORMATION FOR SEQ ID NO:221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

ACTANGTGCA GGTGCGCACA AATATTTGTC GATATTCCTC TCATCTTGGA TTCCATGAGG	60
TCTTTTGCCC AGCCTGTGGC TCTACTGTAG TAAGTTTCTG CTGATGAGGA GCCAGNATGC	120
CCCCCACTAC CTTCCCTGAC GCTCCCCANA AATCACCCAA CCTCTGT	167

(2) INFORMATION FOR SEQ ID NO:222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

AGGGCGTGGT GCGGAGGGCG GTACTGACCT CATTAGTAGG AGGATGCATT CTGGCACCCC	60
GTTCTTCACC TGTCCCCCAA TCCTTAAAAG GCCATACTGC ATAAAGTCAA CAACAGATAA	120
ATGTTTGCTG AATTAAAGGA TGGATGAAAA AAATTAATAA TGAATTTTGG CATAATCCAA	180
TTTTCTCTTT TATATTTCTA GAAGAAGTTT CTTTGAGCCT ATTAGATCCC GGAATCTTT	240
TAGGTGAGCA TGATTAGAGA GCTTGTAGGT TGCTTTTACA TATATCTGGC ATATTGAGT	300
CTCGTATCAA AACAATAGAT TGGTAAAGGT GGTATTATTG TATTGATAAG T	351

(2) INFORMATION FOR SEQ ID NO:223

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

AAAACAAACA AACAAAAAAA ACAATTCCTC ATTACAGAAA ATTATCTTAG GGACTGATAT	60
TGGTAATTAT GGTCAATTTA ATWRTRTTKT GGGGCATTTT CTTACATTGT CTTGACAAGA	120
TTAAAATGTC TGTGCCAAAA TTTTGTATTT TATTTGGAGA CTTCTTATCA AAAGTAATGC	180
TGCCAAAGGA AGTCTAAGGA ATTAGTAGTG TTCCCMTCAC TTGTTTGGAG TGTGCTATTC	240
TAAAAGATTT TGATTTCTTG GAATGACAAT TATATTTTAA CTTTGGTGGG GGAAANAGTT	300
ATAGGACCAC AGTCTTCACT TCTGATACTT GTAAATTAAT CTTTATTGTC ACTTGTTTTG	360
ACCATTAAGC TATATGTTTA AAA	383

(2) INFORMATION FOR SEQ ID NO:224

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224

CCCCTGAAGG CTTCTTGTTA GAAAATAGTA CAGTTACAAC CAATAGGAAC AACAAAAAGA	60
AAAAGTTTGT GACATTGTAG TAGGGAGTGT GTACCCCTTA CTCCCCATCA AAAAAAAAT	120
GGATACATGG TTAAAGGATA RAAGGGCAAT ATTTTATCAT ATGTTCTAAA AGAGAAGGAA	180
GAGAAAATAC TACTTTCTCR AAATGGAAGC CCTTAAAGGT GCTTTGATAC TGAAGGACAC	240
AAATGTGGCC GTCCATCCTC CTTTARAGTT GCATGACTTG GACACGGTAA CTGTTGCAGT	300
TTTARACTCM GCATTGTGAC	320

CLAIMS

1. A method for detecting prostate cancer in a patient, comprising:
 - (a) contacting a biological sample obtained from the patient with a binding agent which is capable of binding to a polypeptide, the polypeptide comprising an immunogenic portion of a prostate protein or a variant thereof, wherein said protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224, the complements of said nucleotide sequences and variants of said nucleotide sequences; and
 - (b) detecting in the sample a protein or polypeptide that binds to the binding agent, thereby detecting prostate cancer in the patient.
2. The method of claim 1 wherein the binding agent is a monoclonal antibody.
3. The method of claim 2 wherein the binding agent is a polyclonal antibody.
4. A method for monitoring the progression of prostate cancer in a patient, comprising:
 - (a) contacting a biological sample obtained from the patient with a binding agent that is capable of binding to a polypeptide, said polypeptide comprising an immunogenic portion of a prostate protein or a variant thereof, wherein said protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224, the complements of said nucleotide sequences and variants of said nucleotide sequences;
 - (b) determining in the sample an amount of a protein or polypeptide that binds to the binding agent;
 - (c) repeating steps (a) and (b); and

(d) comparing the amount of polypeptide detected in steps (b) and (c) to monitor the progression of prostate cancer in the patient.

5. A monoclonal antibody that binds to a polypeptide comprising an immunogenic portion of a prostate protein or a variant thereof, wherein said protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 8-29, 41-45, 47-52, 54-65, 70, 73, 74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209-211, 220, 222-224, the complements of said nucleotide sequences variants of said nucleotide sequences.

6. A method for inhibiting the development of prostate cancer in a patient, comprising administering to the patient a therapeutically effective amount of a monoclonal antibody according to claim 5.

7. The method of claim 6 wherein the monoclonal antibody is conjugated to a therapeutic agent.

8. A method for detecting prostate cancer in a patient comprising:

- (a) obtaining a biological sample from the patient;
- (b) contacting the sample with at least two oligonucleotide primers in a polymerase chain reaction, wherein at least one of the oligonucleotides is specific for a DNA molecule encoding a polypeptide comprising an immunogenic portion of a prostate protein or of a variant thereof, said protein comprising an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224, the complements of said nucleotide sequences variants of said nucleotide sequences; and
- (c) detecting in the sample a DNA sequence that amplifies in the presence of the oligonucleotide primers, thereby detecting prostate cancer.

9. The method of claim 8, wherein at least one of the oligonucleotide primers comprises at least about 10 contiguous nucleotides of a DNA molecule having a sequence selected from SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224.

10. A diagnostic kit comprising:

- (a) one or more monoclonal antibodies of claim 5; and
- (b) a detection reagent.

11. A diagnostic kit comprising:

- (a) one or more monoclonal antibodies that bind to a polypeptide encoded by a DNA molecule having a nucleotide sequence selected from the group consisting of SEQ ID Nos: 5-7, 30-40, 46, 53, 66-69, 71, 72, 75-78, 80, 82-86, 88, 89, 91, 94-96, 98-102, 105, 106, 161-170, 179, 180, 182-187, 189, 190, 192, 195-197, 199-202, 205, 206, 208, 212-219, 221, the complements of said sequences and variants of said nucleotide sequences; and
- (b) a detection reagent.

12. The kit of claims 10 or 11 wherein the monoclonal antibodies are immobilized on a solid support.

13. The kit of claim 12 wherein the solid support comprises nitrocellulose, latex or a plastic material.

14. The kit of claims 10 or 11 wherein the detection reagent comprises a reporter group conjugated to a binding agent.

15. The kit of claim 14 wherein the binding agent is selected from the group consisting of anti-immunoglobulins, Protein G, Protein A and lectins.

16. The kit of claim 14 wherein the reporter group is selected from the group consisting of radioisotopes, fluorescent groups, luminescent groups, enzymes, biotin and dye particles.

17. A diagnostic kit comprising at least two oligonucleotide primers, at least one of the oligonucleotide primers being specific for a DNA molecule encoding a polypeptide comprising an immunogenic portion of a prostate protein or a variant thereof, said protein comprising an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224, the complements of said nucleotide sequences and variants of said nucleotide sequences.

18. A diagnostic kit of claim 17 wherein at least one of the oligonucleotide primers comprises at least about 10 contiguous nucleotides of a DNA molecule having a sequence selected from SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224.

19. A method for detecting prostate cancer in a patient, comprising:

- (a) obtaining a biological sample from the patient;
- (b) contacting the biological sample with an oligonucleotide probe specific for a DNA molecule encoding a polypeptide comprising an immunogenic portion of a prostate protein or a variant thereof, said protein comprising an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224, the complements of said nucleotide sequences and variants of said nucleotide sequences; and
- (c) detecting in the sample a DNA sequence that hybridizes to the oligonucleotide probe, thereby detecting prostate cancer in the patient.

20. The method of claim 19 wherein the oligonucleotide probe comprises at least about 15 contiguous nucleotides of a DNA molecule having a sequence selected from the group consisting of SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224.

21. A diagnostic kit comprising an oligonucleotide probe specific for a DNA molecule encoding a polypeptide comprising an immunogenic portion of a prostate

protein or a variant thereof, said protein comprising an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224, the complements of said nucleotide sequences variants of said nucleotide sequences.

22. The diagnostic kit of claim 21, wherein the oligonucleotide probe comprises at least about 15 contiguous nucleotides of a DNA molecule having a sequence selected from the group consisting of SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224.